

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: GAMBER Examiner #: 7675 Date: 8/7/00
 Art Unit: 1644 Phone Number 308-3997 Serial Number _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: 09/249011 / CO

Inventors (please provide full names): B. L. Als

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

SEQ + SEQ INTERFERENCE SEARCH

SEQ ID NOS 7 - NA

8 - AA

5 - NA

6 - AA

REQUEST
IN
THANK

RECEIVED
AUG - 7 - 2001
TECH/CHM DIVISION
(15131)

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: [Signature] NA Sequence (#) 2 STN _____
 Searcher Phone #: 8128 AA Sequence (#) 2 Dialog _____
 Searcher Location: _____ Structure (#) _____ Questel/Orbit _____
 Date Searcher Picked Up: 8/7 Bibliographic _____ Dr. Link _____
 Date Completed: 8/28 Litigation _____ Lexis/Nexis Chapman 8/7 - 6⁰⁰ - 1068 - 1072
 Searcher Prep & Review Time: _____ Fulltext _____ Sequence Systems MBI 8/15 - 6⁰⁰ - 1055 - 1063
 Clerical Prep Time: 15 Patent Family _____ WWW/Internet 8/10 - 6⁰⁰ - 1053 - 1057
 Online Time: 20 Other _____ Other (specify) 8/11 - 6⁰⁰ - 1053 - 1057
8/14 - 6⁰⁰ - 1053 - 1057
8/15 - 6⁰⁰ - 1053 - 1057
8/16 - 6⁰⁰ - 875 - 882
8/17 - 6⁰⁰ - 856 - 860
8/18 - 6⁰⁰ - 632 - 636
8/19 - 6⁰⁰ - 455 - 463
8/21 - 6⁰⁰ - 292 - 296
8/22 - 6⁰⁰ - 228 - 232

PTO-1590 (1-2000)

8/23 - 6⁰⁰ - 174 - 178
 8/24 - 6⁰⁰ - 171 - 175
 8/26 - 6⁰⁰ - 93 - 97
 8/27 - 6⁰⁰ - 1K

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 05:41:38 ; Search time 838.43 Seconds

(without alignments)
862.090 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405

Sequence: 1 atgggttggaactgtatcat.....ccctgtcacgcgtctctca 405

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_da1:*

2: gb_da2:*

3: gb_om:*

4: gb_om:*

5: gb_pat:*

6: gb_ph:*

7: gb_pl1:*

8: gb_pl2:*

9: gb_pl1:*

10: gb_pl2:*

11: gb_pl3:*

12: gb_ro:*

13: gb_sy:*

14: gb_sy:*

15: gb_un:*

16: gb_un:*

17: em_fun:*

18: em_hum1:*

19: em_hum2:*

20: em_om:*

21: em_om:*

22: em_om:*

23: em_ov:*

24: em_pat:*

25: em_ph:*

26: em_pl:*

27: em_ro:*

28: em_sy:*

29: em_sy:*

30: em_un:*

31: em_vl:*

32: gb_htg1:*

33: gb_htg2:*

34: gb_in1:*

35: gb_in2:*

36: em_da1:*

37: em_da2:*

38: em_hum3:*

39: em_hum4:*

40: gb_pi4:*

41: gb_pi3:*

42: gb_pi2:*

43: gb_pi1:*

44: gb_pi0:*

44: gb_pi0:*

45: em_htg1:*

46: em_htg2:*

47: em_htg3:*

48: em_hum5:*

49: gb_pi3:*

50: gb_pi4:*

51: gb_pi5:*

52: gb_pi6:*

53: gb_pi7:*

54: gb_pi8:*

55: gb_pi9:*

56: gb_pi10:*

57: gb_pi11:*

58: gb_pi12:*

59: gb_pi13:*

60: gb_pi14:*

61: gb_pi15:*

62: gb_pi16:*

63: gb_pi17:*

64: gb_pi18:*

65: gb_pi19:*

66: gb_pi20:*

67: gb_pi21:*

68: gb_pi22:*

69: gb_pi23:*

70: gb_pi24:*

71: gb_pi25:*

72: gb_pi26:*

73: gb_pi27:*

74: gb_pi28:*

75: gb_pi29:*

76: gb_pi30:*

77: gb_pi31:*

78: gb_pi32:*

79: gb_pi33:*

80: gb_pi34:*

81: gb_pi35:*

82: gb_pi36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272.2	67.2	446	5	108288 Sequence 4
2	272.2	67.2	462	12	S78361
3	251.4	62.1	405	9	HSIGHX11
4	248.2	61.3	433	5	AR024343 Sequence
5	248.2	61.3	433	5	AR045196 Sequence
6	245	60.5	405	5	I31950 Sequence 68
7	245	60.5	405	5	I78562 Sequence 68
8	245	60.5	405	5	I78617 Sequence 68
9	245	60.5	405	9	HSBUD114H
10	245	60.5	405	12	MUSIGHM195
11	243.4	60.1	405	5	E16346
12	243.4	60.1	405	5	E14571
13	241.8	59.7	414	11	AF062257
14	241.8	59.7	451	12	MUSANTVDJ
15	241.8	59.7	471	12	MUSANTVDJ
16	241.2	59.6	700	12	MUSIGHMO
17	241.2	59.6	700	12	MUSIGHMO
18	240.2	59.3	402	9	HSVHTB6
19	240.2	59.3	406	12	MUSIGHMX
20	240.2	59.3	443	5	I09505 Sequence 3
21	239.2	59.1	466	12	MMIGRF24
22	239	59.0	418	5	E16338
23	239	59.0	418	5	E16335
24	239	59.0	462	9	HUMIGHVAL

108288 Sequence 4

S78361 AHT107 VH r

X65893 H.sapiens m

AR024343 Sequence

AR045196 Sequence

I31950 Sequence 68

I78562 Sequence 68

I78617 Sequence 68

Z46348 Homo sapien

M83098 Mus musculu

E16346 DNA encodin

E14571 Mouse mRNA

AF062257 Homo sapi

M37621 Mouse anti-

M27788 Mouse Ig ac

J00494 Mouse Ig ac

M25465 Mouse Ig re

Z47222 H.sapiens m

M28251 Mouse Ig re

I09505 Sequence 3

X14623 Murine MRL-

E16328 DNA coding

E16335 DNA coding

M18512 Human (feta

25	238.6	58.9	433	5	I31929	Sequence 18
26	238.6	58.9	433	5	I78541	Sequence 18
27	238.6	58.9	433	5	I78596	Sequence 18
28	237.6	58.7	422	5	AR033861	Sequence
29	237.6	58.7	422	5	AR033835	Sequence
30	237.6	58.7	422	5	AR042495	Sequence
31	237.6	58.7	422	5	AR058375	Sequence
32	237.4	58.6	418	5	E16326	DNA coding
33	237.4	58.6	418	5	E16332	DNA coding
34	237.4	58.6	418	5	E16334	DNA coding
35	237.4	58.6	418	5	E16336	DNA coding
36	237	58.5	405	9	HS1GHXX37	H.sapiens m
37	237	58.5	411	9	HSVH1R10	H.sapiens m
38	237	58.5	452	9	HSE551A15	H.sapiens r
39	236.8	58.5	409	23	E11590	endocdi
40	236.8	58.5	484	12	MUS1GH4C11	Mouse tGR
41	236.8	58.5	490	12	MUS1G4C11A	Mouse ant1
42	235.8	58.2	418	5	E16330	DNA coding
43	235.8	58.2	418	5	E16333	DNA coding
44	235.6	58.2	420	11	AF067121	Homo sap
45	235.6	58.2	417	11	AF0663208	Homo sap

ALIGNMENTS

[illegible]

Db	345	GAACCTGGCCAGATTGACATCTGAAATATCTCCACATCTTACTGTGCAAGA	---	GGANGC	401
Oy	361	tatatgactactgggtcgaaggtacccctgtgcacgtccctca	405		
Db	402	AACCTTGACTACTGGGGCCAAAGCACCACTCTCACAGTCTCTCA	446		
RESULT	2				
LOCUS	S78361	462 bp	mRNA	ROD	07-MAY-1993
DEFINITION	AH107 VH region-chimeric mouse/human MAb against the human p55 IL-2R heavy chain variable region [mice, mRNA Recombinant Partial, 462 nt].				
ACCESSION	S78361				
VERSION	S78361.1	GI:243052			
KEYWORDS					
SOURCE	Mus sp.				
ORGANISM	Mus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 462) Rose, B., Gillespie, A., Wunderlich, D., Barbosa, J.A., Cahill, K., Dzau, J., Shedd, D. and Zierler, B. A chimeric mouse/human anti-IL-2 receptor antibody with enhanced biological activities Mol. Immunol. 29 (1), 131-144 (1992) 92114885 GenBank staff at the National Library of Medicine created this entry [NCBI gidsq 78361] from the original journal article. This sequence comes from Fig1B. Location/Qualifiers 1..462 /organism="Mus sp." /db_xref="taxon:10095" 1..462 /partial /gene="AH107 VH region" 61..462 /partial /gene="AH107 VH region" /note="chimeric mouse/human MAb against the human p55 IL-2R heavy chain variable region; this sequence comes from Fig1B. /codon_start=1 /product="AH107 VH region" /protein_id="AAB21040.1" /db_xref="GI:243053" /translation="MGWSCIILFLAATATSYHSOVYQOQSGPEYVRPGVSYSKICKSSGYLTEDYLAHWKQSHAKSLSEIGIISYNGDYSINPRFKATMTVDKSSSTAYMELARLSEDSAIYVCAKRGSNLDYMGGTLTVSS"				
BASE COUNT	122 a	112 c	118 g	110 t	
ORIGIN					
Query Match	67.2%;	Score 272.2;	DB 12;	Length 462;	
Best Local Similarity	81.2%;	Pred. No. 8.3e-76;			
Matches 329;	Conservative	0;	Mismatches 73;	Indels 3;	Gaps 1;
Oy	1	atggttgggaactgtatcatactcttcttctgtgttaccacagctacaggtgtgcaactccag	60		
Db	61	ATGGCTGGAGCTGTATCATCTCTTCTTGCGCAGCAACAGCTACAACTGTGCACCTCCAG	120		
Oy	61	gtcagcgtgtgtcaatctcgtgggtcgtgaagtgaagaagctcgtggaagctcgtgaaggtgcc	120		
Db	121	GTCCAGCTGCACACACTCTGGGCTTAGGGTGGGAAGCCTGGGGTTCAGTGAAGATTTC	180		
Oy	121	tgcagaacttcgcggtacacattcactactattatgtatcacagttggttgaagaagctcct	180		
Db	181	TGCAAGGCTTCGGCTACACATTCATGATTTGCTCTGCACTGGGTGAAGCAGATCAT	240		
Oy	181	ggacagggctcgaattgattgagttatataattactatgtataataacactcaac	240		

Db	241	GCAAGACTCTAAGATGATGGATTGCAGTAATTATTAAGTTCCTACAAATGGTGATTACAGCTAAC	300
Oy	241	cagaagtttaaggccaagccacaatgactctgttagacaagtgcacagcacaagcctatatg	300
Dd	301	CCGAGCTTTTAAGGGCACAAGGCCACCATGTACTGTATAACAATCTCTCCACACAGCCTATATG	360
Oy	301	gaacttagtctcttgagatctgagataagcgcttattactctgtgaagaagcgacctg	360
Db	361	GAACTTGCCACATTGACATCTGAAGAATTCTGCCATCTTAATTACTGTGAAGA---GGAAGC	417
Oy	361	tataatgactactgggtgcaagtagaccctcttcgacgctctccca	405
Db	418	AACCTTAGCTACTGGGGCCAAGCACCAACCTCTACAGTCTCTCTCA	462
RESULT	3		
LOCUS	HSIGHXX11		
DEFINITION	H.sapiens mRNA for XLA Ig heavy chain VDJ region (LE 1-9).	PRI	26-JUL-1997
ACCESSION	X65893.5S9756		
VERSION	X65893.1 GI:395090		
KEYWORDS	diversity region; Ig heavy chain; immunoglobulin; joining region; variable region.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Schiff,C.		
JOURNAL	Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE		
REFERENCE	2 (bases 1 to 405)		
AUTHORS	Mallil,M., Le Deist,F., de Saint-Basile,G., Fischer,A., Fougereau,M. and Schiff,C.		
TITLE	Bone marrow cells in x-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire		
JOURNAL	J.Clin. Invest. 91 (4), 1616-1629 (1993)		
MEDLINE	9332287		
FEATURES			
source	Location/Qualifiers		
	1..405		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/chromosome="14"		
	/tissue_type="bone marrow"		
	/cell_type="pre-B"		
	/clone_id="LE library"		
	/clone="LE 1-9"		
	1..57		
	sig_peptide		
	58..352		
	/note="variable region"		
	misc_feature		
	353..366		
	/note="diversity region"		
	misc_feature		
	367..405		
	/note="joining region"		
	BASE COUNT	95 a 106 c 120 g 84 t	
	ORIGIN		
Query Match	62.1%; Score 251.4; DB 9; Length 405;		
Best Local Similarity	76.3%; Pred. No. 3,4e-69;		
Matches 309; Conservative 0; Mismatches 96; Indels 0; Gaps			
Oy	1 atggagttggaactctatcatctctctcttgtttacacagctacaggtgtgactccag	60	
Dd	1 ATGAGACTGAGACTCGAGAGGTCCTCTTTTGGTGACACAGCCACAGAGTGCCACTCCAG	60	
Oy	61 gtccagcttgctgcagctctggggctcgaagtgaaagagccttggaaggtgtc	120	
Dd	61 GTCCAGCTTTGTCAGATCTGGGGCTGAGGTGAAGAGCCTGGGGCTCAGTGAAGGTTTC	120	

QY	121	tgcaagcttcgcggtacacattccattatgatactacagtgtagagagctcct	180
Db	121	TCGAAGGGCTTGTGGATACACCTTCACCTGACATGCTAATGCAATTGGGTCCGGCCAGCCCCC	180
OY	181	ggacaggccctccagatgtagtggaggttatatacttatctatgataatacaactacaac	240
Db	181	GGACAAAGGCTTGAATGGATGGATGGATTCACACCTGGCAATGTGTAACACAAATATTCA	240
OY	241	cagaagtttaaggggcaagggccaatgactgctgtaagaagtcgacgagcacagccataatg	300
Db	241	CAGAAGTTTCAAGGGGCAAGGTACACCTATTCACAGGAGACATCCGCGACGACGACCTTACATG	300
OY	301	gaacttagttcttcttgatgactctgagagatacgcgcgttttacttgatgcaagagcgcttgg	360
Db	301	GAGCTGACACGCTTGATGATCTGTAAGACACAGCGGTGTGTATTACTGTGTCGACAGAGTAAACC	360
OY	361	tatatgactactggtggtcgaaggtacccctgttcacgctctcctca	405
Db	361	TATTGACTACTGGGGGCCAGGAAACCTGTGTACCGCTTCTCTCA	405
RESULT	4		
LOCUS	AR024343	433 bp	DNA
DEFINITION	Sequence 111 from patent US 5795965.		PAT
ACCESSION	AR024343		
VERSION	AR024343.1	GI:3977637	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 433)		
AUTHORS	Tsuchiya, M., Sato, K., Bendig, M. Margaret, Jones, S. Tarrian and Saidha, J. William.		
TITLE	Reshaped human to human interleukin-6 receptor		
JOURNAL	Patent: US 5795965-A 111 18-AUG-1998;		
FEATURES	Location/Qualifiers		
source	1..433		
	/organism="unknown"		
BASE COUNT	94 a 108 c 128 g 103 t		
ORIGIN	.		
Query Match	61.3%; Score 248.2; DB 5; Length 433;		
Best Local Similarity	75.8%; Pred. No. 3.6e-68;		
Matches 307; Conservative	0; Mismatches 98; Indels 0; Gaps 0;		
OY	1	atggatggaactgtatcatctctcttcttggttacacagctacagtggtgactccag	60
Db	16	ATGGACTGTGACTGGAGGGCTTCTTCTTGTGGCTGTGAGTCCAGCGTCCACACCCAG	75
OY	61	gtccgcgtggtgcacatcctgggggctgtagtgaagaagcctggtagctgaagtgtcc	120
Db	76	GTGCGAGCTTGTGCACTCTGGAGCTGAGGTGAAGAAAGCCTGGGGCCTCAGTGAAGGTTTC	135
OY	121	tgcaagcttcgcggtacacattccattatgatactacagtgagtgtagacagctcct	180
Db	136	TGCAAGGCTTGTGGATACCTTCATCTCAGTTATTATACATACACTGGGTGCGCAGGCCCC	195
OY	181	ggacaggccctccagatgtagtggaggttatatacttatctatgataatacaactacaac	240
Db	196	GGACAAAGGCTTGAATGGATGGATTTTGGACCTTTCAATGGGTGATCTAGCTATTAAT	255
OY	241	cagaagtttaaggggcaagggccaatgactgctgtaagaagtcgacgagcacagccataatg	300
Db	256	CAGAAGTTTCAAGGGGCAAGGTACACCTATTCACAGGAGACATCCGCGACGACACCTTACATG	315
OY	301	gaacttagttcttcttgatgactctgagagatacgcgcgttttacttgatgcaagagcgcttgg	360
Db	316	GAGCTGACACGCTTGATGATCTGTAAGACACAGCGGTGTGTATTACTGTGTCGACAGAGGGGTAAAC	375
OY	361	tatatgactactggtggtcgaaggtacccctgttcacgctctcctca	405

Db 376 CGCTTGTACTGAGGCGCAGGAACCTGTGACCGTCTCTCA 420

RESULT 5 AR045196 433 bp DNA PAT 29-SEP-1999

LOCUS AR045196 Sequence 111 from patent US 5817790.

ACCESSION AR045196

VERSION AR045196.1 GI:5966661

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 433)

AUTHORS Tsuchiya, M., Sato, K., Bendig, M., Margaret, Jones, S., Tarran and Saldanha, J. William.

TITLE Reshaped human antibody to human interleukin-6 receptor

JOURNAL Patent: US 5817790-A 11 06-OCT-1998;

FEATURES Location/Qualifiers

source 1..433

BASE COUNT 94 a 108 c 128 g 103 t

ORIGIN

Query Match 61.3%; Score 248.2; DB 5; Length 433;

Best Local Similarity 75.8%; Pred. No. 3.6e-68;

Matches 307; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Db 1 atgggttggaactgtatcatcttcttcttggttacacagctacaggtgtgacccag 60

15 ATGGAGTGGACCTGGAGGGCTCTCTCTGCTGCTGTGAGCTCCAGGTCTCTCCAG 75

Qy 61 gtccagctgtgcaagctcgtggcgtgagtgaaagcctggagctcagtgaaagtgtcc 120

76 GTGCACCTGTGCAAGCTGAGTGAAGTGAAGAACCTGGGGCTCAAGTGAAGGTTCC 135

Qy 121 tgcgaagcttcgcgtacacattcactgattatgtctatacagtggtgagacagctcct 180

136 TGCAGGCTTCTGGATACATTCATTACTAGTATTATACATACAGGCTGGCCGCCCC 195

Qy 181 ggaacagggcctcgtgagttgagttgagttatataattactatgataatacaactacaac 240

196 GGACAAAGGCTTGAGTGGATATGAGTATGACCTTTCGAATGAGTGTACTACTATAT 255

Qy 241 cagaagtttaagggcagagcccaatgactgtagacaaagtgcagagcagcattatg 300

256 CAGAACTTCAAGGGCAGAGTCAACATTACCTGTAGACACATCCCGAGCACAGCCTACATG 315

Qy 301 gaactagttcttgagactgagatacagagtaagcgccttattactgtgcaagagcgctcg 360

316 GAGCTGAGCAGTCTGAGATCTGAGACAGCGCTGTATTACTGTGCGAGAGGGGTAAAC 375

Qy 361 tatatgactactggtggtcaaggtacacctgtcacacctctca 405

376 CGCTTGTACTGAGGCGCAGGAACCTGTGACCGTCTCTCA 420

RESULT 6

LOCUS I31950 405 bp DNA PAT 06-FEB-1997

DEFINITION Sequence 68 from patent US 5585089.

ACCESSION I31950

VERSION I31950.1 GI:1822741

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 405)

AUTHORS Queen, C.L. and Selick, H.E.

TITLE Humanized immunoglobulins

JOURNAL Patent: US 5585089-A 68 17-DEC-1996;

FEATURES Location/Qualifiers

source 1..405
/organism="unknown"

BASE COUNT 101 a 106 c 105 g 93 t

ORIGIN

Query Match 60.5%; Score 245; DB 5; Length 405;

Best Local Similarity 75.3%; Pred. No. 3.7e-67;

Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 1 atgggttggaactgtatcatcttcttcttggttacacagctacaggtgtgacccag 60

15 ATGGAGTGGACCTGGAGGGCTCTCTCTGCTGCTGTGAGCTCCAGGTCTCTCCAG 60

Qy 61 gtccagctgtgcaagctcgtggcgtgagtgaaagcctggagctcagtgaaagtgtcc 120

61 GTGCACCTGTGCAAGCTGAGTGAAGTGAAGAACCTGGGGCTCAAGTGAAGGTTCC 120

Qy 121 tgcgaagcttcgcgtacacattcactgattatgtctatacagtggtgagacagctcct 180

121 TGCAGGCTTCTGGATACATTCATTACTAGTATTATACATACAGGCTGGCCGCCCC 180

Qy 181 ggaacagggcctcgtgagttgagttgagttatataattactatgataatacaactacaac 240

181 GGAAAGAGCCTTGAGTGGATATGAGTATGATCTTCAATGAGTGTACTGTGCTAAC 240

Qy 241 cagaagtttaagggcagagcccaatgactgtagacaaagtgcagagcagcattatg 300

241 CAGAACTTCAAGGGCAGAGTCAACATTACCTGTAGACACATCCCGAGCACAGCCTACATG 300

Qy 301 gaactagttcttgagactgagatacagagtaagcgccttattactgtgcaagagcgctcg 360

301 GAGCTGAGCAGTCTGAGATCTGAGACAGCGCTGTATTACTGTGCGAGAGGGGTAAAC 360

Qy 361 tatatgactactggtggtcaaggtacacctgtcacacctctca 405

361 GCTATGAGTACTGAGGCGCAGGAACCTGTGACCGTCTCTCA 405

Db 361 GCTATGAGTACTGAGGCGCAGGAACCTGTGACCGTCTCTCA 405

RESULT 7

LOCUS I78562 405 bp DNA PAT 03-APR-1998

DEFINITION Sequence 68 from patent US 5693761.

ACCESSION I78562

VERSION I78562.1 GI:3014716

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 405)

AUTHORS Queen, C.L., Schneider, W.P. and Selick, H.E.

TITLE Polynucleotides encoding improved humanized immunoglobulins

JOURNAL Patent: US 5693761-A 68 02-DEC-1997;

FEATURES Location/Qualifiers

source 1..405

BASE COUNT 101 a 106 c 105 g 93 t

ORIGIN

Query Match 60.5%; Score 245; DB 5; Length 405;

Best Local Similarity 75.3%; Pred. No. 3.7e-67;

Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 1 atgggttggaactgtatcatcttcttcttggttacacagctacaggtgtgacccag 60

15 ATGGAGTGGACCTGGAGGGCTCTCTCTGCTGCTGTGAGCTCCAGGTCTCTCCAG 60

Qy 61 gtccagctgtgcaagctcgtggcgtgagtgaaagcctggagctcagtgaaagtgtcc 120

61 GTGCACCTGTGCAAGCTGAGTGAAGTGAAGAACCTGGGGCTCAAGTGAAGGTTCC 120

Qy 121 tgcgaagcttcgcgtacacattcactgattatgtctatacagtggtgagacagctcct 180

Db 121 TGCAGGCTTCGTGATACATTCTAGCTACATCAACATGCACTGGGTGAAGCAGACCAT 180
Oy 181 ggacgggcccgcgagtgatggatggaattatattactactaagaatacaactacaac 240
Db 181 ggaaagacccttgatgagatgatatatttcttaccAAAGGGGAGACTGCTCAAC 240
Oy 241 cagaagtttaagggcaagggcccaatgactgagacaagtcgaagcagacagccataty 300
Db 241 CAGAAGTTCAGAGAGCAAGGCCACATTGACTGTAGACAATTCTCCAGCACACCTTACATG 300
Oy 301 gaacttaattcttgagatctgagatacagcgcttattactgtgcaagagcgcccttg 360
Db 301 GACGTCCCGACGCTCACAATCTGAGACACCTGCAAGTCTATTACTGTGCAAGAGGGGCCCC 360
Oy 361 tatatgactactgggtgcaagtgacccctgtcacccgtctcctca 405
Db 361 GCTATGACTACTGGGTCAAGGAACCTCAGTCAACCGTCTCTCA 405

RESULT 8
LOCUS 178617 405 bp DNA PAT 03-APR-1998
DEFINITION Sequence 68 from patent US 5693762.
ACCESSION 178617
VERSION 178617.1 GI:3014771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 405)
AUTHORS Queen,C.L., Co,M.Sung, Schneider,W.P., Landolfi,N.F., Coelinhg,K.L.
TITLE Humanized immunoglobulins
JOURNAL Patent: US 5693762-A 68 02-DEC-1997;
FEATURES Location/Qualifiers
source 1..405
BASE COUNT 101 a 106 c 105 g 93 t
ORIGIN

Query Match 60.5%; Score 245; DB 5; Length 405;
Best Local Similarity 75.3%; Pred. No. 3.7e-67;
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Oy 1 atgggttggaactgtatcatcttcttctgtgttaccacaagctacaggtgtgactccag 60
Db 1 ATGGGATGAGCTGATCTTCTCTCTCCGTGACGAACTGCAAGGCGTCCACTCTGAG 60
Oy 61 gtccagctgggagcgtctggggctgagtgaaagaagcctggagctcagtgaaagtgtcc 120
Db 61 GTCCAGCTTTCAGACATCAGGACCTGAGCTGTGAACCTGGGGCCTCACTGAAGATATCC 120
Oy 121 tgcagaagcttcgcggtacacattcactgatactgatacagtggtgagacagctcct 180
Db 121 TGCAGGCTTCGTGATACATTCTAGCTACATCAACATGCACTGGGTGAAGAGCCAT 180
Oy 181 ggaacgggctcgagtgagtgagtgatattactactatgataataatacaactacaac 240
Db 181 GGAAGGACCTTGATGATGATGATATTATCTTACAAATGAGTGTGACTGGCTAACAAC 240
Oy 241 cagaagtttaagggcaagggcccaatgactgagacaagtcgaagcagacagccataty 300
Db 241 CAGAAGTTCAGAGAGCAAGGCCACATTGACTGTAGACAATTCTCCAGCACACCTTACATG 300
Oy 301 gaacttaattcttgagatctgagatacagcgcttattactgtgcaagagcgcccttg 360
Db 301 GACGTCCCGACGCTCACAATCTGAGACACCTGCAAGTCTATTACTGTGCAAGAGGGGCCCC 360
Oy 361 tatatgactactgggtgcaagtgacccctgtcacccgtctcctca 405
Db 361 GCTATGACTACTGGGTCAAGGAACCTCAGTCAACCGTCTCTCA 405

RESULT 9
LOCUS HSBUD114H 405 bp mRNA PRI 27-OCT-1994
DEFINITION Homo sapiens mRNA for anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b).
ACCESSION 246348
VERSION 246348.1 GI:560839
KEYWORDS anti-Sm antibody; diversity region; immunoglobulin heavy chain; joining region; variable region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 405)
AUTHORS Primates; Catarrhini; Homnidae; Homo.
TITLE Mahmoudi,M., Edwards,J., Cairns,E. and Bell,D.
JOURNAL Molecular characterization of natural human anti-Sm autoantibodies unpublished
REFERENCE 2 (bases 1 to 405)
AUTHORS Mahmoudi,M.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-1994) Mahmoudi M., University of Western Ontario, Medicine and Microbiology and Immunology, University Hospital Room BRE-12, London, Ontario, Canada, N6A 5A5
FEATURES Location/Qualifiers
source 1..405
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="BUD114"
/tissue-type="human tonsil"
/cell-type="B-cell"
sig_peptide 1..57
CDS 1..>405
/codon_start=1
/product="anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b)"
/protein_id="CA86467.1"
/db_xref="GI:560840"
/translation="MDWTWRILFLVMAATGAHSOVLVQSAEYKRPASVYCKSKAS
GYTFGTIMRWKQAPGQGLMMKMINSGITVNAQDFQGRVTMTROTSTISTAMEL
SLRSDPTAVYVCARARTGYNMGQGLTVSS"
58..351
/gene="hVH1L1"
/note="VH segment"
58..351
/gene="hVH1L1"
352..366
/note="D region/close to DK1 and DM1 germline genes"
367..405
/note="JH4b region"
BASE COUNT 92 a 107 c 128 g 78 t
ORIGIN

Query Match 60.5%; Score 245; DB 9; Length 405;
Best Local Similarity 75.3%; Pred. No. 3.7e-67;
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Oy 1 atgggttggaactgtatcatcttcttctgtgttaccacagctacaggtgtgactccag 60
Db 1 ATGGAAGTTCAGAGAGCAAGGCCACATTGACTGTAGACAATTCTCCAGCACACCTTACATG 60
Oy 61 gtccagctgggagcgtctggggctgagtgaaagaagcctggagctcagtgaaagtgtcc 120
Db 61 GTCCAGCTTTCAGACATCAGGACCTGAGCTGTGAACCTGGGGCCTCACTGAAGATATCC 120
Oy 121 tgcagaagcttcgcggtacacattcactgatactgatacagtggtgagacagctcct 180
Db 121 TGCAGGCTTCGTGATACATTCTAGCTACATCAACATGCACTGGGTGAAGAGCCCAT 180
Oy 181 ggaacgggctcgagtgagtgagtgatattactactatgataataatacaactacaac 240
Db 181 GGACAAAGGCGCTTGATGATGATGATATTATCTTACAAATGAGTGTGACTGGCTAACAAC 240

Oy	241	cagaagtttaaggccaagggccacaaatgactgtgaacaagctcgaccagcagacctataty	300
Dd	241	CAGAAgTTTCAGGGCCAGGCGTACCATATACCAGGCAACGTCTCATTACGACACAGCCTTAAATG	300
Oy	301	gaacttagtctcttgagactcbagagatacagccggtattatctagtgcagaagcgyacctg	360
Dd	301	GAGCTGAGCACAGCTGAACAATCTGACGACACAGCGCGTGATTAATCTGTGCAGAGGCTTAGACT	360
Oy	361	tatatgacctactiggggtcaaggraacctctgtcatccttcacca	405
Dd	361	GGATTAATACTACTGGGGCCAGGACACCTTGCTACCGTCTCTCTCA	405
RESULT	10		
LOCUS	MUSIGHM195		
DEFINITION	Mus musculus Ig heavy chain mRNA V-region, from hybridoma M195		
ACCESSION	M83098		
VERSION	M83098.1 GI:195613		
SOURCE	V-region; Immunoglobulin; Immunoglobulin heavy chain.		
ORGANISM	Mus musculus hybridoma M195 CDNA to mRNA.		
REFERENCE	Mus musculus		
AUTHORS	Eukaryotes: Metazoa: Chordata: Craniata: Vertebrata: Mammalia: Euthetia: Rodentia: Sciurognathi: Muridae: Murinae: Mus. 1 (bases 1 to 403) Co.M.S., Avdalovic,N.M., Caron,P.C., Avdalovic,M.V., Schelberg,D.A. and Queen,C. Chimeric and humanized antibodies with specificity for the CD3 antigen		
JOURNAL	J. Immunol.	148,	1149-1154 (1992)
MEDLINE	92148135		
FEATURES	Location/Qualifiers		
SOURCE	1..403		

sig_peptide	1..60	/gene="Igh"
		/note="putative"
CDS	1..405	/partial
		/gene="Igh"
		/note="V-region; putative"
		/codon_start=1
		/product="immunoglobulin heavy chain"
		/protein_id="AAA38370.1"
		/db_xref="GI:195614"
		/translation="MGMSWIFLFLISGPAVSEYOLQSGPELVKPAASYKSKAS
		GYTFDDNMHWKSHGSKSLFMIGIYIPYNGCTYQNKFRKATILTYDNSSITAMDV
		RSLSIEDSAVYICARGPAMDYWGCGISVTSS"
gene	1..405	
		/gene="Igh"
		61..405
		/gene="Igh"
		/note="V-region"
		/product="immunoglobulin heavy chain"
BASE COUNT	101 a 106 c 105 g 93 t	
ORIGIN		

Query Match	60.5%	Score 245;	DB 12;	Length 405;
Best Local Similarity	75.3%	Pred. No. 3.7e-67;		
Matches 305;	Conservative 0;	Mismatches 67;	Indels 0;	Gaps 0;
0y	1 atgggttggaactgcatctctcttcctggttacacagcctgaggtgacccag	60		
Db	1 ATGGGATGGAGCTGATCTTCTCTCTCCCTCGTAGGAACTGCAAGGCTCCACCTGAG	60		
0y	61 gtccagctctgtctatctctgggctgagctgaaagccctggagagctcaagtgtccc	120		
Db	61 GTCCAGCTTCAACCAAGTCAGGACCTGAGGCTGTGAACCTGGGGCCCTCATGTGAAGTATCC	120		

Oy	121	tgcgaagcttcggcgctacacattccacgattatgctctaaagctgggtggaagagctcc	180
Oy	121	tcgaagcttcggcgctacacattccacgattatgctctaaagctgggtggaagagctcc	180
Db	121	TGCAGAGCTTTGGATACACATTACTGACTACACACATGCACTGGGTGAAGCAGACCAT	180
Oy	181	ggacaagggcctcgatcgatggattggaattataattactatgataataacaatacaac	240
Db	181	GGAAGAAGCCTTGGATGGATGGATATATTATTCCTTCACATGCTGGTATCTGCCTCAAC	240
Oy	241	cagaagtttaagggacaagggccacaatactactgtaagaagtcgagcgggacaagctatag	300
Oy	241	CAGAGTTTCAGAGCAAGGCCACATTACTGTAGACATTCTTCACACAGCCTTCATG	300
Db	241	CAGAGTTTCAGAGCAAGGCCACATTACTGTAGACATTCTTCACACAGCCTTCATG	300
Oy	301	gaacttagttcttggagaatctgagatatacgcgtttattactgtgcagaagcggcgctgg	360
Oy	301	GACGCCACACCTCGACATCTGAGAGACTCTGCAGTCTATACTGTGCAAGAGGGGCCCC	360
Db	301	GACGCCACACCTCGACATCTGAGAGACTCTGCAGTCTATACTGTGCAAGAGGGGCCCC	360
Oy	361	tatatgactactagggtcaagagacacctgttaacgcttcctccca	405
Oy	361	tatatgactactagggtcaagagacacctgttaacgcttcctccca	405
Db	361	GCTATGGACTCTGGGGTCAAGAGACCTTCAGTACCGCTTCCTCTCA	405

RESULT	11
LOCUS	E16346
DEFINITION	DNA encoding immunoglobulin VH region of anti-human Fas mouse monoclonal antibody CH11.
ACCESSION	E16346
VERSION	E16346.1 GI:5711029
KEYWORDS	JP 1998165178-A/9.
SOURCE	Mus sp.
ORGANISM	Mus sp. Eumetazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 405)
AUTHORS	Shibata,M and Watanabe,Y.
TITLE	DNA ENCODING VARIABLE REGION OF ANTI-FAS ANTIBODY AND ANTI-FAS
JOURNAL	PATENT: JP 1998165178-A-23-JUN-1998;
COMMENT	IGAKU SEIBUTSUGAKU KENKYUSHO:KK Mus sp. (mouse) Mus sp. (mouse)

PD	23-JUN-1998				
PF	01-JUL-1997	JP	1997191769		
PR	02-JUL-1996	JP	96P	172228,	09-OCT-1996 JP 96P 268737 PI
SHIBAHARA MASAO,	WATANABE YUKO				
PC	CI2N15/00,	C07K16/18,	CI2P21/02,	(CI2P21/02, CI2P1:91);	CC
strandedness: Double;					
CC	topology: linear;				
FH	Key		Location/Qualifiers		
FT	source		1..405		
FT			/organism="Mus sp. '		
FT			/cell-type="hybridoma"		
FT			/cell_line="Ch11"		
FT	sig-peptide		1..57		
FT	V-region		58..405.		
Location/Qualifiers					
	1..405				
	/organism="Mus sp. "				
	/db_xref="taxon:10095"				
BASE COUNT	103 a	102 c	102 g	98 t	
ORIGIN					

	Query Match	Similarity	60.1%	Score	243.4	DB 5:	Length	405:	
	Best Local	Similarity	75.1%	Pred.	No. 1,2=66:				
	Matches	304;	Conservative	0;	Mismatches	101;	Indels	0; Gaps	0
OY	1	atgggttggaactgctatcaattccttccttgcgtttaccacagactcacggttgtcaactccag	60						
Db	1	ATGGGATGGAGGTGGATCTTCTCTCCCTCGTAGAGACATGCAGGCCCTCCACTTTGAG	60						
OY	61	gtccacgctctgttcagtctctgggctctgaagtgaagaagccctgggagctccagtgaaagtgtccc	120						

BASE COUNT	454 a	513 c	417 g	389 t
ORIGIN	/db_xref="taxon:10090"			
Query Match	60.1%;	Score 243.4;	DB 5;	Length 1773;
Best Local Similarity	75.1%;	Pred. No. 1.5e-66;		
Matches 304;	Conservative 0;	Mismatches 101;	Indels 0;	Gaps 0;
Oy	1	atgggttggaactgatactctctctctctggttaccacagctacagatggtgcactccag	60	
Db	1	ATGGGATGGAGCTGGATCTTTCTCTCTCCCTCGTCAGGAACCTGCAGGGCTCCACTCTGAG	60	
Oy	61	gtccagctggtgacagctctggggcttgaagtgaaagccctgggaagctcagtgaaagtgtcc	120	
Db	61	GTCCAGCTTTCAGCAGCTCAGGAGCTGAGCTGGTGAAGCAACCTGGGGCTCAGTGAAGATATCC	120	
Oy	121	tgcgaagcttcgggtacacattcacttaattatgtatatacagtggtgtgagaaagctcct	180	
Db	121	TGCAAGGCTTCTGGATACACATTCAGTCAATCAACATGCACTGGGTGAAGCAGGCCAT	180	
Oy	181	ggacaggggcctcogaaatggatgtgaatttaataattactatgataatacaaacatacaac	240	
Db	181	GGAAGAGACCTTGATGGATGGATGGATATATTTATCTTACATAGTGGTGGTACTGGCTACAC	240	
Oy	241	cagaagttaaggaggaagggccacaatgaactgaactgaagcaagtcgagcagacagacccatata	300	
Db	241	CAGAAGTTCAGAGCAGCAAGCAGCACATTTGACTGTGACAAATTCCTCCAGCAGACGCTTACATG	300	
Oy	301	gaacttagtctcttgatgtctgagatacagcgccttattactgtgcgaagcgagcctgg	360	
Db	301	GAGCTCCCGAGCCTGACATCTGAGGACTCTGAGTCTTATCTGTGTCAGGAAGATTACTAT	360	
Oy	361	tatatgactactggtggcgaaggtacacctgtgcacgctctctca	405	
Db	361	GCTATGGACTACTGGGGTCAAGGAACCTCAGTACCGTCTCTCA	405	
RESULT 13				
AF062257	414 bp	mRNA	PR1	02-JUN-1998
LOCUS				
DEFINITION	Homo sapiens clone Xu-12 immunoglobulin heavy chain variable region			
ACCESSION	AF062257			
VERSION	AF062257.1			
KEYWORDS	GI:3170980			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	1 (bases 1 to 414)			
JOURNAL	Wang, X. and Stollar, B.D.			
AUTHORS	unpublished			
TITLE	2 (bases 1 to 414)			
JOURNAL	Wang, X. and Stollar, B.D.			
AUTHORS	Direct Submission			
TITLE	Submitted (24-APR-1998)			
JOURNAL	Biochemistry Department, Tufts University			
AUTHORS	SCHOOL OF Medicine, 136 Harrison Ave., Boston, MA 02111, USA			
TITLE	Location/Qualifiers			
FEATURES	1. .414			
SOURCE	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/chromosome="14"			
	/map="14q32.33"			
	/clone="Xu-12"			
	/cell_type="peripheral B lymphocyte"			
	/tissue_type="blood"			
	/note="from young repertoire Xu"			
	1. .>414			
	/gene="IGH"			
	1. .>414			
CDS				

```

/ gene="IGH"
/ product="immunoglobulin heavy chain variable region"
/ protein_id="A018293.1"
/ db_xref="GI:3170981"
/ translation="MDMTWRIILFLVAATGAHSQVQLVDSGAEVKKPSQVSCKAS
GYFTGVMHVRQAGGLEMMGMINPAAKFGKQRTMTKDISIPAYMEL
SRLRSDDTAVYCAFTAGAAAYFYWGQGLTVYVSSG"
sig_peptide
1..57
/ gene="IGH"
/ protein_id="A018293.1"
/ db_xref="GI:3170981"
BASE COUNT 91 a 111 c 132 g 80 t
ORIGIN

Query Match 59.7% Score 241.8; DB 11; Length 414;
Best Local Similarity 76.2% Pred. No. 3.9e-66;
Matches 313; Conservative 0; Mismatches 92; Indels 6; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgttaccacagctagagtggtgactccag 60
DB 1 ATGGAGTGGAGCTTGAGATCTCTCTCTGTGGCAGCAGCAGAGGCCACTCCAG 60
QY 61 gtccagctgtgcaagctctgagctgaggaagcctggaagcctgagtgagtgctcc 120
DB 61 GTCCAGCTGTGCGAGCTGTGGGCGTGAAGAGCCTGGGGCTCAGTGAAGTCTCC 120
QY 121 tgcgaagcttcgggtacacattcagatgatacagctggtgagacaggtcct 180
DB 121 TGCAAGGCTTCTGGATACACCTTCACCGGCTACTATATGACTGGGTGCGACAGGCCCT 180
QY 181 ggaaagggcctcgagtgatgagtgatataatattatgataataataataataac 240
DB 181 GGAAAGGGCTTGAGTGGATGGATGGATACCCCTTAACCTGATGGCACAATATGCA 240
QY 241 cagaagtttaagggaagccacaaatgactgtagaagaagtcgaagcagacagctatg 300
DB 241 CAGAAGTTTACGGGCAAGGATACCATGACAGGACAGTGCATACAGACAGCTACATG 300
QY 301 gaacttgatcttggagatcagagatacggcgcttattactgtgcgaagacggcctg 359
DB 301 GAGCTGAGCAGGCTGAGATCTGACGACACGCGCTGATTTACTGTGCGAGACAGCGGA 360
QY 360 -----gtaataagactactgtggcgaagatgacccctgtcacgctcctca 405
DB 361 GCTGCTATTATTGACTACTGGGCGCAGGAGACCTGGTCCGCTCTCA 411

RESULT 14
MUSANTVDJ 451 bp DNA ROD 29-OCT-1994
LOCUS MUSANTVDJ
DEFINITION Mouse anti-DNA autoantibody variable region, diversity region, and
Joining region.
ACCESSION M37621
VERSION M37621.1 GI:293302
KEYWORDS D-region; J-region; V-region; anti-DNA autoantibody.
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Kofler,R., Noonan,D.J., Levy,D.E., Wilson,M.C., Moller,N.P.,
Dixon,F.J. and Theofilopoulos,A.N.
Genetic elements used for a murine lupus anti-DNA autoantibody are
closely related to those for antibodies to exogenous antigens
J. Exp. Med. 161 (4), 805-815 (1985)
JOURNAL MEDLINE
FEATURES
source
1..451
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"

/ gene="IGH"
/ product="immunoglobulin heavy chain variable region"
/ protein_id="A018293.1"
/ db_xref="GI:3170981"
/ translation="MDMTWRIILFLVAATGAHSQVQLVDSGAEVKKPSQVSCKAS
GYFTGVMHVRQAGGLEMMGMINPAAKFGKQRTMTKDISIPAYMEL
SRLRSDDTAVYCAFTAGAAAYFYWGQGLTVYVSSG"
sig_peptide
1..57
/ gene="IGH"
/ protein_id="A018293.1"
/ db_xref="GI:3170981"
BASE COUNT 110 a 113 c 117 g 111 t
ORIGIN

Query Match 59.7% Score 241.8; DB 12; Length 451;
Best Local Similarity 74.8% Pred. No. 3.9e-66;
Matches 303; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatcttcttctgttaccacagctagagtggtgactccag 60
DB 47 ATGGAGTGGAGCTTGATCATCTCTTTTGTGAGCAGCAGCTCAGTGTCCAGC 106
QY 61 gtccagctgtgcaagctctgagctgaggaagcctggaagcctgagtgagtgctcc 120
DB 107 GTCCAGCTGTGCGAGCTGTGGGCGTGAAGAGCCTGGGGCTCAGTGAAGCTGTCC 166
QY 121 tgcgaagcttcgggtacacattcagatgatacagctggtgagacaggtcct 180
DB 167 TGCAAGGCTTCTGGATACACCTTCACCGGCTACTATATGACTGGGTGCGACAGGCCCT 226
QY 181 ggaaagggcctcgagtgatgagtgatataatattatgataataataataataac 240
DB 227 GGAAAGGGCTTGAGTGGATGGAAATATTATTCCTGTGATGATGATGATGATGAT 286
QY 241 cagaagtttaagggaagccacaaatgactgtagaagaagtcgaagcagacagctatg 300
DB 287 GAGAAAGTTCAAGGACAGGCGACACACTGACTGACACACTCTCCAGCAGCCTCATG 346
QY 301 gaacttgatcttggagatcagagtgatataatattatgataataataataataac 360
DB 347 CAGCTCAGCAGCCTGAGATCTGAGACTGTGCGCTATTATGTTGCAAGATTGATGCA 406
QY 361 tataatgactacagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 405
DB 407 GGGTTCTTACTTGGGCGCAAGGAGCTGTGCTACTGCTCTCTCA 451

RESULT 15
MUSIGHPG 471 bp mRNA ROD 27-APR-1993
LOCUS MUSIGHPG
DEFINITION Mouse Ig active mu-chain mRNA V-D-J2-C region, clone 18C10.
ACCESSION M27788
VERSION M27788.1 GI:195851
KEYWORDS C-region; D-region; J-region; V-region; immunoglobulin heavy chain;
immunoglobulin mu-chain; processed gene.
SOURCE Mouse spleen, cDNA to mRNA, clone 18C10.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 471)
Kaartinen,M., Rocca-Serra,J. and Maekela,O.
Combinatorial association of V genes: One V-H gene codes for three
non-cross-reactive monoclonal antibodies each specific for a
different antigen (phoxalone, NP or GAT)
Mol. Immunol. 25, 859-865 (1988)
JOURNAL MEDLINE
FEATURES
source
1..471
/organism="Mus musculus"
/ db_xref="taxon:10090"
/ protein_id="AA38441.1"
/ translation="MGMSCTMLFLAATGVSQVQLVDSGAEVKKPSQVSCKAS
GYFTSVMHVRQAGGLEMMGMINPAAKFGKQRTMTKDISIPAYMEL"
sig_peptide
49..105
/ note="Ig mu-chain signal peptide"
491..>471
/ note="Ig mu-chain V-D-J2-C region precursor"

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 05:31:28 ; Search time 864.98 Seconds
(without alignments)
2064.765 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405
Sequence: 1 atgggtgtgaactgtatcat.....ccctgtcacgcgtccctca 405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

```
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_est45:*
80: gb_est46:*
81: gb_est47:*
82: em_est35:*
83: em_est36:*
84: em_est37:*
85: gb_est48:*
86: gb_est49:*
87: gb_est50:*
88: gb_est51:*
89: gb_est52:*
90: gb_est53:*
91: gb_est54:*
92: gb_est55:*
93: gb_gss1:*
94: gb_gss2:*
95: gb_gss3:*
96: gb_gss4:*
97: em_gss1:*
98: em_gss2:*
99: em_gss3:*
100: em_gss4:*
101: gb_gss5:*
102: gb_gss6:*
103: gb_gss7:*
104: gb_gss8:*
105: gb_gss9:*
106: em_gss5:*
107: em_gss6:*
108: em_gss7:*
109: em_gss8:*
110: em_gss9:*
111: em_gss10:*
112: em_gss11:*
113: gb_gss10:*
114: gb_gss11:*
115: em_gss12:*
116: gb_gss12:*
```

```
117: qb_gss13: *
118: qb_gss14: *
119: qb_gss15: *
120: qb_gss16: *
121: qb_gss17: *
122: qb_gss18: *
123: qb_gss19: *
124: em_gss13: *
```

Result	Score	Query Match	Length	DB	ID	Description
--------	-------	-------------	--------	----	----	-------------

C	45	188.6	46.6	528	44	A1799757	AM403591	UI-HF-BKO	AM408371	488	72	AM408371	226	56.0	488	72	AM408371	1
	1	224	55.3	417	72	AM402081	AM402081	UI-HF-BKO	AM402081	488	72	AM402081	224	55.3	417	72	AM402081	2
	2	220.8	54.5	488	44	A1791363	AM402081	UI-HF-BKO	AM402081	488	44	A1791363	220.8	54.5	488	44	A1791363	3
	3	220	54.3	513	72	AM402081	AM402081	UI-HF-BKO	AM402081	513	72	AM402081	220	54.3	513	72	AM402081	4
	4	219.8	54.3	516	72	AM402422	AM402422	UI-HF-BKO	AM402422	516	72	AM402422	219.8	54.3	516	72	AM402422	5
	5	218.8	54.0	477	72	AM408484	AM408484	UI-HF-BKO	AM408484	477	72	AM408484	218.8	54.0	477	72	AM408484	6
	6	218.2	53.9	587	72	AM403728	AM403728	UI-HF-BKO	AM403728	587	72	AM403728	218.2	53.9	587	72	AM403728	7
	7	218.2	53.9	587	72	AM403728	AM403728	UI-HF-BKO	AM403728	587	72	AM403728	218.2	53.9	587	72	AM403728	8
	8	215.6	53.2	510	72	AM403806	AM403806	UI-HF-BKO	AM403806	510	72	AM403806	215.6	53.2	510	72	AM403806	9
	9	215.2	53.1	498	72	AM403294	AM403294	UI-HF-BKO	AM403294	498	72	AM403294	215.2	53.1	498	72	AM403294	10
	10	215	53.1	449	72	AM402364	AM402364	UI-HF-BKO	AM402364	449	72	AM402364	215	53.1	449	72	AM402364	11
	11	214.4	52.9	527	72	AM402139	AM402139	UI-HF-BKO	AM402139	527	72	AM402139	214.4	52.9	527	72	AM402139	12
	12	213	52.6	485	72	AM403940	AM403940	UI-HF-BKO	AM403940	485	72	AM403940	213	52.6	485	72	AM403940	13
	13	212.6	52.5	438	72	AM630198	AM630198	UI-HF-BKO	AM630198	438	72	AM630198	212.6	52.5	438	72	AM630198	14
	14	212.4	52.4	457	72	AM408270	AM408270	UI-HF-BKO	AM408270	457	72	AM408270	212.4	52.4	457	72	AM408270	15
	15	211.8	52.3	542	72	AM405977	AM405977	UI-HF-BKO	AM405977	542	72	AM405977	211.8	52.3	542	72	AM405977	16
	16	211.6	52.2	419	72	AM402189	AM402189	UI-HF-BKO	AM402189	419	72	AM402189	211.6	52.2	419	72	AM402189	17
	17	208.2	51.4	488	72	AM402665	AM402665	UI-HF-BKO	AM402665	488	72	AM402665	208.2	51.4	488	72	AM402665	18
	18	207.6	51.3	387	28	AA569186	AA569186	UI-HF-BKO	AA569186	387	28	AA569186	207.6	51.3	387	28	AA569186	19
	19	207.6	51.3	501	72	AM402603	AM402603	UI-HF-BKO	AM402603	501	72	AM402603	207.6	51.3	501	72	AM402603	20
	20	207.2	51.2	466	72	AM403202	AM403202	UI-HF-BKO	AM403202	466	72	AM403202	207.2	51.2	466	72	AM403202	21
	21	206	50.9	460	72	AM406939	AM406939	UI-HF-BKO	AM406939	460	72	AM406939	206	50.9	460	72	AM406939	22
	22	205.6	50.8	508	72	AM403684	AM403684	UI-HF-BKO	AM403684	508	72	AM403684	205.6	50.8	508	72	AM403684	23
	23	204.6	50.5	457	72	AM405627	AM405627	UI-HF-BKO	AM405627	457	72	AM405627	204.6	50.5	457	72	AM405627	24
	24	201.8	49.8	371	72	AM403410	AM403410	UI-HF-BKO	AM403410	371	72	AM403410	201.8	49.8	371	72	AM403410	25
	25	201.4	49.7	361	36	A1201426	AM402942	UI-HF-BKO	A1201426	361	36	A1201426	201.4	49.7	361	36	A1201426	26
	26	200.8	49.6	466	72	AM402942	AM402942	UI-HF-BKO	AM402942	466	72	AM402942	200.8	49.6	466	72	AM402942	27
	27	200.2	49.4	391	79	AM630635	AM630635	UI-HF-BKO	AM630635	391	79	AM630635	200.2	49.4	391	79	AM630635	28
	28	200.2	49.4	474	72	AM405180	AM405180	UI-HF-BKO	AM405180	474	72	AM405180	200.2	49.4	474	72	AM405180	29
	29	199.8	49.3	321	64	AM130201	AM130201	UI-HF-BKO	AM130201	321	64	AM130201	199.8	49.3	321	64	AM130201	30
	30	199	49.1	435	72	AM402541	AM402541	UI-HF-BKO	AM402541	435	72	AM402541	199	49.1	435	72	AM402541	31
	31	198.6	49.0	412	72	AM403256	AM403256	UI-HF-BKO	AM403256	412	72	AM403256	198.6	49.0	412	72	AM403256	32
	32	198.6	49.0	453	46	A1923980	AM630630	UI-HF-BKO	A1923980	453	46	A1923980	198.6	49.0	453	46	A1923980	33
	33	198.4	49.0	429	79	AM630630	AM630630	UI-HF-BKO	AM630630	429	79	AM630630	198.4	49.0	429	79	AM630630	34
	34	198	48.9	477	72	AQ462845	AQ462845	UI-HF-BKO	AQ462845	477	72	AQ462845	198	48.9	477	72	AQ462845	35
	35	197.8	48.8	486	72	AM403686	AM403686	UI-HF-BKO	AM403686	486	72	AM403686	197.8	48.8	486	72	AM403686	36
	36	197.6	48.8	400	79	AM630968	AM630968	UI-HF-BKO	AM630968	400	79	AM630968	197.6	48.8	400	79	AM630968	37
	37	197.2	48.7	331	72	AM407729	AM407729	UI-HF-BKO	AM407729	331	72	AM407729	197.2	48.7	331	72	AM407729	38
	38	195.4	48.2	418	72	AM401468	AM401468	UI-HF-BKO	AM401468	418	72	AM401468	195.4	48.2	418	72	AM401468	39
	39	193.6	47.8	312	72	AM401829	AM401829	UI-HF-BKO	AM401829	312	72	AM401829	193.6	47.8	312	72	AM401829	40
	40	193.6	47.8	416	72	AM402457	AM402457	UI-HF-BKO	AM402457	416	72	AM402457	193.6	47.8	416	72	AM402457	41
	41	192.8	47.6	344	72	AM403535	AM403535	UI-HF-BKO	AM403535	344	72	AM403535	192.8	47.6	344	72	AM403535	42
	42	191.4	47.3	343	72	AM402227	AM402227	UI-HF-BKO	AM402227	343	72	AM402227	191.4	47.3	343	72	AM402227	43
	43	190.8	47.1	356	72	AM405552	AM405552	UI-HF-BKO	AM405552	356	72	AM405552	190.8	47.1	356	72	AM405552	44
	44	190.2	46.6	437	79	AM629597	AM629597	UI-HF-BKO	AM629597	437	79	AM629597	190.2	46.6	437	79	AM629597	45
	45	188.6	46.6	528	44	A1799757	AM403591	UI-HF-BKO	A1799757	528	44	A1799757	188.6	46.6	528	44	A1799757	C

LOCUS	488 bp	EST	16-FEB-2000
DEFINITION	UI-HF-BKO-abg-b-01-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone		
IMAGE:3056184	5', mRNA sequence.		

VERSION	AM403591	GI:6922577
ACCESSION	AM403591	GI:6922577
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
AUTHORS	1 (bases 1 to 488)	
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bdrrp/image/image.html Seq primer: M13 Forward.	
FEATURES	Location/Qualifiers	
SOURCE	1..488 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3056184" /clone_1id="NIH_MGC_36" /tissue_type="lymph" /cell_type="germinal center B cells" /cell_line="MGC85" /lab_host="DH10B (LTI)" /note="Vector: pRT3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Benito Soares, Ph.D."	
BASE COUNT	111 a 136 c 140 g 101 t	
ORIGIN		
Query Match	56.0%; Score 226.6; DB: 72; Length 488;	
Best Local Similarity	73.5%; Pred. No. 1.5e-58;	
Matches 311; Conservative	0; Mismatches 94; Indels 18; Gaps 1;	
QY	1 atgggttggaactgcatctctctctctctgtgttaccacagctacagtggtgcaccag 60	
Db	2 ACGAGGTGACTGAGAGATCTCTTTTGGTGGCAGACGCCACAGTCCCATCCAG 61	
QY	61 gtccagctgtgcaactctcgtggcttgaagtgaaagacgctcggagctcagtgaaagtgtcc 120	
Db	62 GTCCAGCTTGTGCAAGTCTGGGGCTGAGGTGAAGAACGCTGGGGCCTCAGTGAAGTTTCC 121	
QY	121 tgcgaagcttcgcgtctaacatctcaactgtatgtatatacagtggtgtgaagagctctc 180	
Db	122 TGCAGGCTTGTGATACCTTCACATCACTACATGCTATATACATTTGGTCCGCCAGCCGCC 181	
QY	181 ggacagggccctcggatgttgaggttataatctatctacttgataatcaactacaac 240	
Db	182 GGACAAAGGCTTGAAGTATGGATGATGATCAACGCTGGCAATAGTATACACAAATATTCA 241	
QY	241 cagaagtttaagggcacaagccacaatgactgtagaacaagtcgacgacagacagcctatag 300	
Db	242 CAGAAGTTTCAAGGGGAGAGTCACCATTTGCCAGGGGACACATCCGGAGACAGACCTACATG 301	
QY	301 gaacttagctcttgagatctgagatacggccggttattctactgttgcagaagcg----- 354	
Db	302 GAGCTGACACACTCGATCTGTAAGACACAGCGCTGTATTACTGTGCGAGAGCGGAGAAAT 361	
QY	355 -----gctgttatatgactacactcggggtcaagtgatccctgttaccgtctcc 402	
Db	362 TACTATGTTGATGAGGAGTCTCTTGTGACTACATGGGGGCCAGGGAACCTTGATACCGTCTCC 421	

Query Match	54.3%	Score 220:	DB 72:	Length 513:
Best Local Similarity	76.3%	Pred. No. 1.6e-56:		
Matches 284; Conservative	0;	Mismatches 85;	Indels 3;	Gaps 1;
Qy	34	accacagctacaaagtgctgacactccaggtccagctgctgacagctgctgagctgagctgagctgag	93	
Db	2	ACGAGGGGCTACAGGTGTCCAGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAG	61	
Qy	94	aagcctgagagctcaaggaaggtgtctctgcaaaagcttcgcgactacacattacattattat	153	
Db	62	AAGCCTGGGCTCCTAAGTGAAGGTCTCCGCAAGGCTTTGAGGACCTTACAGCAGCTAT	121	
Qy	154	gctatcacagtggtgagagacagctccctctgagacagagcctcgaattgagttggaattaat	213	
Db	122	GCTATCACCTGGGTGTCGACAGGCCCTCTGACAAAGGCTGTAGTGGATGGAAAGATCATG	181	
Qy	214	attactatgataataacaaatacaacccaagaatttaaggccaagccaatagctgta	273	
Db	182	CCTATCTTGTATACAGCAAGCTACCCACAGAAAGTTCCAGGCGACAGTACAGATTCACCGG	241	
Qy	274	gacaagctgacagagacagcagctcatatgtaactgttcttgaagtctcgaagatagcggc	333	
Db	242	CACAAATCCAGACACACGCTACATGAGCTGACACACCTGAGATCTGAGGACACAGGCG	301	
Qy	334	gttattactgtgcaagagcgagcctggtatatagtactactggtggtcgaagtgtaacctgtc	393	
Db	302	GTGATTTACTCTGCGAGAGAGAGGGGAGTGGCTGG---TCTGGGCGCAGAGGAACCTGGTTC	358	
Qy	394	acgcgtctctca	405	
Db	359	ACCGTCTCTCA	370	
RESULT 5				
LOCUS	AM402422	516 bp	mRNA	EST
DEFINITION	UI-HF-BK0-aan-c-12-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone			IMAGE:3054335, mRNA sequence.
ACCESSION	AM402422			
VERSION	AM402422.1	GI:6921108		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 516)			
JOURNAL	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	On Sep 10, 1999 this sequence version replaced gi:5865948.			
	Contact: Robert Strausberg, Ph.D.			
	Tel: (301) 496-1550			
	Email: Robert.Strausberg@nih.gov			
	Eco RI site shown at the beginning of the sequence.			
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.			
	cDNA Library Preparation: M.B. Soares Lab			
	cDNA Library Arrayed by: M.B. Soares Lab			
	DNA Sequencing by: M.B. Soares Lab			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/BLN at:			
	www-bio.lnl.gov/bbrp/image/image.html			
	Seq primer: M13 Forward			
FEATURES	Location/Qualifiers			
SOURCE	1..516			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:3054335"			
	/clone_1lb="NIH_MGC_36"			
	/tissue_type="lymph"			
	/tissue_type="germinal center B cells"			
	/cell_line="MGC85"			

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3056487"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTR)"
/note="Vector: pRT3-Pac; Site.1: NotI; Site.2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonald, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 135 a 177 c 157 g 118 t
ORIGIN

Query Match 53.9%; Score 218.2; DB 72; Length 587;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 268; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatctctcttcttggttacacagctacaggtgtgctccag 60
DB 52 ATGGAGCTGGACCTGGAGCTCTTTCTTGTGGCAGCAGCAACAGTCCACCTCCAG 111
QY 61 gtccagctgtgagctctggtggtggaagagcctggagctcagtgaggtctc 120
DB 112 GTTCAGCTGGTCACTGTGAGCTGAGTGAGAACCTGGGGCTCAGTGAAGTCTCC 171
QY 121 tgcagaagcttcggtcaccatctacatgtatgtatcagtggtgagagagctct 180
DB 172 TCAGAGGCTTGTTGTTACCTTTACCACTTATGAGATCTGGTGGCAGAGGCCCT 231
QY 181 ggcagagggcctgagtggttggtatataattactatgatatcaactaac 240
DB 233 GGACAGAGGCTTGAGTGAGTGAGTACCGCTTACAAATGATTAACAATATGCA 291
QY 241 cagaagtttaaggcagaagccacaatgactgtagacaagctgacagcagcctatag 300
DB 292 CAGAGGCTTCAGAGGCGAGATCAACCGTACACAGACACATCCAGCAGCAGCTCAAG 351
QY 301 gaactagttcttgagatctgagatagatagacgcgcttattactgtgcaaga 351
DB 352 GAAGTGGAGGCTGAGATCCAGCACACAGCGCGTGTATTACTGTGCGAGA 402

RESULT 8
AM403806 510 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BK0-abn-b-12-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3056615 5', mRNA sequence.
ACCESSION AM403806
VERSION AM403806.1 GI:6922851
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 510)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN at:
www.bto.llnl.gov/btrp/image/image.html

Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1..510
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3056615"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTR)"
/note="Vector: pRT3-Pac; Site.1: NotI; Site.2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonald, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 112 a 140 c 151 g 107 t
ORIGIN

Query Match 53.2%; Score 215.6; DB 72; Length 510;
Best Local Similarity 71.8%; Pred. No. 3.4e-55;
Matches 306; Conservative 0; Mismatches 99; Indels 21; Gaps 1;

QY 1 atgggttggaactgtatcatctctcttcttggttacacagctacaggtgtgctccag 60
DB 28 ATGGAGCTGGACCTGGAGATCTCTTTTGTGGCAGCAGCAGCAGCTCCAG 87
QY 61 gtccagctgtgagctctggtggtggaagagcctggagctcagtgaggtctc 120
DB 88 GTTCAGCTGGTCACTGTGAGCTGAGTGAGAACCTGGGGCTCAGTGAAGTCTCC 147
QY 121 tgcagaagcttcggtcaccatctacatgtatgtatcagtggtgagagagctct 180
DB 148 TCAGAGGCTTGTTGTTACCTTTACCACTTATGAGATCTGGTGGCAGAGGCCCT 207
QY 181 ggcagagggcctgagtggttggtatataattactatgatatcaactaac 240
DB 208 GGAGAAAGGCTTGATGATGATGATGATGATCAACGCTGGCAATGATTAACAATATGCA 267
QY 241 cagaagtttaaggcagaagccacaatgactgtagacaagctgacagcagcctatag 300
DB 268 CAGGAGTTCAGAGGCGAGATCAACCGTACACAGCAGCAGCAGCAGCTCAAG 327
QY 301 gaactagttcttgagatctgagatagatagacgcgcttattactgtgcaaga 360
DB 328 GAGCTGAGCAGCTGAGATCTGAGACGCTGCTGTATTATTGTGCGAGAGAGGTTAC 387
QY 361 tat-----atgactactgtgggtcagaaggtaccctgtgacgctc 399
DB 388 GATTTTGGAGTGTATTATACCTTTTGACTACTGTGGGCGAAGGAACCTGTACCGTC 447
QY 400 tccctca 405
DB 448 TCCTCA 453

RESULT 9
AM402294 498 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BK0-aag-f-06-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3054083 5', mRNA sequence.
ACCESSION AM402294
VERSION AM402294.1 GI:6920980
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 498)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

IMAGE:3055588 5', mRNA sequence.
ACCESSION AM402139
VERSION AM402139.1 GI:6920825
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
TITLE Unpublished (1999)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL On Mar 8, 1999 this sequence version replaced gi:438206.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1..527
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3055588"
/clone_1lb="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTI)"
/note="Vector: p7773-Pac. Site.1: NotI; Site.2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 113 a 155 c 156 g 103 t
ORIGIN
Query Match 52.9%; Score 214.4; DB 72; Length 527;
Best Local Similarity 75.6%; Pred. No. 7.9e-55;
Matches 266; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1 atgggttggaactgtatcatcttcttctgtgtacacagctacaggtgtgcactccag 60
DB 14 ATGGACTGGACCTGGAGGCTTCTTGTGGTGAGAGCTACAGGTGTGCTCCAG 73
QY 61 gtccagctgtgtcagctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
DB 74 GTCCAGCTGTGTGAGCTGTGGGCTGTGAGGTGAAGAACTGTGTGTGTGTGTGT 133
QY 121 tgcgaagcttcggtcactcattcattgtatgtatgtatgtatgtatgtatgtat 180
DB 134 TGCAAGGCTTCTGGAGGACCTTCACAGGATTCCTATCAGCTGGGTGCACAGGCCCT 193
QY 181 ggaacaggtcctcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
DB 194 GGACAGGCTTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 253
QY 241 cagaagtttaaggcgaagcgaacatgtatgtatgtatgtatgtatgtatgtatgt 300
DB 254 CAGAACTTCAGACAGAGACAGATTCACGCGAGCAAGATTCACAGAGCAGCCTACAT 313
QY 301 gaactagtcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 352
DB 314 GACCTAGCAGCCTGTGGATCTGTAGACACGCGCTGTATTACTGTGAGAG 365

RESULT 12
LOCUS AM403940
DEFINITION UT-HF-BKO-abn-h-01-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056881 5', mRNA sequence.
ACCESSION AM403940
VERSION AM403940.1 GI:6922908
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
TITLE Unpublished (1999)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL On May 7, 1998 this sequence version replaced gi:3119607.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1..485
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3056881"
/clone_1lb="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTI)"
/note="Vector: p7773-Pac. Site.1: NotI; Site.2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 101 a 135 c 152 g 97 t
ORIGIN
Query Match 52.6%; Score 213; DB 72; Length 485;
Best Local Similarity 75.1%; Pred. No. 2.1e-54;
Matches 283; Conservative 0; Mismatches 85; Indels 9; Gaps 1;
QY 38 cagctacaggtgtgtcactccaggtccagctgtgtgtgtgtgtgtgtgtgtgtgt 97
DB 12 CAGCTACAGGTGTGTGCTCCAGGTCCAGCTGTGTGTGTGTGTGTGTGTGTGTGT 71
QY 98 ctggaggtcctcaatgaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 157
DB 72 CTGGGTCTCTGGAGAGGTCTCTGCAAGGCTTGTGAGGACCTTCACAGCTTACTA 131
QY 158 tacagtggttgagacaggtcctctgtgacaggtcctcagtgatgtgtgtatatt 217
DB 132 TCAGCTGGGTGTGAGAGGCGCTGTGAGCAAGGCTTGTAGTGTGTGTGTGTGTGT 191
QY 218 actatgataatacaactcaacaaagtttaaggcgaagccacaaatgtatgtaga 277
DB 192 TCTTTATCAACAAGATGTGTGCAAGAAATTCACAGGAGAGTTCAGATTCACAGAG 251
QY 278 agtcgagcggcagacgtctatgtgaactagtcttctgtgtgtgtgtgtgtgtgt 337
DB 252 AGCTTACAGCAGCAGCTTACAGAGTGTGAGAGCCTGTGAGTGTGAGACAGCCGT 311
QY 338 attactgtgcaagag-----cggtgtgtatagtactgtgtgtgtgtgtgtgt 388


```

Db 312 ATTAGTGGCGAGAGAGGGCTTTTGGAGTGGCTTTGACTGAGGCGCAGGAAACC 371
Qy 389 ttgtacagctctctca 405
Db 372 TGGTCACCGCTCTCTCA 388

RESULT 13
AM630198 438 bp mRNA EST 31-MAR-2000
LOCUS hm19g07.y1 NCI-CCAP.GU1 Homo sapiens cDNA clone IMAGE:2969052 5'
DEFINITION similar to gp:M8789 IG GAMMA-1 CHAIN C REGION (HUMAN);, mRNA
sequence.
ACCESSION AM630198
VERSION AM630198.1 GI:7376988
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Oct 19, 1998 this sequence version replaced gi:2442188.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/resources.shtml
Seq primer: -40RP from Glibco
High quality sequence stop: 422.
FEATURES
source Location/Qualifiers
1..438
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2969052"
/clone_lib="NCI-CCAP.GU1"
/tissue_type="2 pooled high-grade transitional cell
tumors"
/lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: PCMV-SPORT6;
Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Library constructed by Life
Technologies."
BASE COUNT 104 a 121 c 125 g 87 t 1 others
ORIGIN
Query Match 52.5%; Score 212.6; DB 79; Length 438;
Best Local Similarity 73.1%; Pred. No. 2.7e-54;
Matches 272; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 1 atgggttggaactgtatctcttcttctgtgtaccacagctgagtgatccacag 60
Db 44 ATGACACTCAGCTGGAGATCTCTTCTTGTGGCAGCAGCTACAGGACCCAGCCAG 103

Qy 61 gtccagctgtgtcagctctgtgggtctgaaggctgtgagagctcagtgaggcttc 120
Db 104 GTCACAGCTGTGACACTGTGGGACTGAGGTGAAGAGCCCTGGGCTCACTGAGGTCTCC 163

Qy 121 tgcgaagcttcgggtctaacatctcattatgtctatacagtggtgtgaagacagctct 180
Db 164 TGCAGGTTTCCGGGTGACCCCTCAGTGAATTATTCATGCACTGGGTGCGAGAGCTCTCT 223

```

```

Qy 181 ggcagagcctcagtgatgtgattatattactatgatataatacaactacaac 240
Db 224 GGAGAGAGGCTTGAGTGGATGGAGAGTGTGATCTTGAAGATGGGAAACACTCTACGA 283

Qy 241 cagaagtttaaggcgaagccacaatgactgtagaacagtcgacagacacccattatg 300
Db 284 CAGAAGTTCACAGCGCAGAGTCCACATGACCCGAGACACATCTACAGACACACCTCATATG 343

Qy 301 gactagtctcttgatgtatgagatagcgcgtttattatctgtgcaagagcgctgg 360
Db 344 AACTGAGCAGCCTGATATCTGAAGACAGCGCGTATATTACTGTGTAAACANGACTGGG 403

Qy 361 tatcagagctac 372
Db 404 GATCGAAGCTTC 415

RESULT 14
AM408270 517 bp mRNA EST 16-FEB-2000
LOCUS UT-HF-BK0-abj-b-07-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3056221 5', mRNA sequence.
ACCESSION AM408270
VERSION AM408270.1 GI:6927327
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL On Jan 6, 2000 this sequence version replaced gi:6677324.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
FEATURES
source Location/Qualifiers
1..517
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3056221"
/clone_lib="NIH_MGC_36"
/tissue_type="1 lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTR)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Benito Soares, Ph.D."
BASE COUNT 106 a 156 c 156 g 99 t
ORIGIN
Query Match 52.4%; Score 212.4; DB 72; Length 517;
Best Local Similarity 77.2%; Pred. No. 3.2e-54;
Matches 258; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 19 atctctcttcgtgtaccacagctacaggtgtgcacccaggtccagctgtgtgagctct 78
Db 10 ATCCTCTTCTGTGGCAGACGACAGGAGGCCACTCCAGGTCGACACTGGTGCAGTCT 69

```



```

Db 214 GCAAGAGCTAGAGTGGATTGAGTATTAGTCTAGCTGCGAGACAAACATACAC 273
Qy 241 cagaagtttaaggcgaagccacaatgactgttagacaagtgcagcagccatattg 300
Db 274 CAGAGTTTAAAGGAGAGCCACAAATGACTGTTGACAAATCTCCAAACACCTATTGG 333
Qy 301 gaactagttcttgaagatcgaagataagcgcgttattactgtgcagaagcgccttg 360
Db 334 GAACATTGCCAGATTGACATCTGAGGATTGTGCCATCTATTACTGTGCAAGAGGGGATGG 393
Qy 361 -----tatatgactactcgtgggtcaaggtacacctgtcacgcctctca 405
Db 394 TTACTACTCTCTCTTGTGACTACTGCGGCCAAGGACACACTCTCAGACTCTCTCA 447

```

RESULT 2
Q14652
ID Q14652 standard; cDNA: 524 BP.
AC Q14652;

DT 14-FEB-1992 (first entry)
DE R6-5-D6 anti-ICAM-1 heavy chain.
KW Interleukin-2 receptor molecule-1; antibody; chimeric; ds.
OS Mus musculus.

FT Key Location/Qualifiers
FT signal_peptide 34..90
FT cds /*tag= a
FT /*tag= b

FN WO9116928-A.
PN 14-NOV-1991.
PR 29-APR-1991; U02946.
PR 27-APR-1990; GB-009548.
PA (CELL-) CELLTECH LTD.
PA (BOHR) BOEHRINGER INGELHEIM PHA.
PI Adair JR, Robinson MK, Bright SM, Rothlein RA;
DR WPI: 91-353534/48.
DR P-PSDB: R15200.

PT New humanised chimeric anti-ICAM-1 antibodies - useful in treating inflammation e.g. psoriasis and ulcerative colitis to suppress metastasis of haematopoietic tumour cell and in diagnosis.

PS Claim 10; Fig 2; 85pp; English.

CC The sequence comprises the 5' untranslated region, signal sequence, variable region and part of the constant region for the R6-5-D6 murine Mab heavy chain. The hybridoma cell line R6-5-D6 producing the anti-ICAM-1 Ab was provided by Boehringer Ingelheim Pharmaceuticals Inc. The cells were grown and mRNA isolated and used to prepare cDNA for a library in pSP64 vector DNA. The library was grown in E. coli IM1035 and colonies screened using a probe complementary to a sequence in the mouse kappa constant region or with a 980 bp BamHI-EcoRI restriction fragment of a previously isolated mouse IgG2a constant region clone. Ten CC positive clones were isolated and rescreened. Positive clones from the second round of screening were grown and the DNA inserts sequenced. The DNA was used to construct a humanised Abs having CC chimeric variable regions, esp. with IgG human constant region CC domains. The Abs can be used to treat inflammation, to suppress CC metastasis of haematopoietic tumour cells and growth of ICAM-1 CC expressing tumour cells, to treat viral infection, to suppress CC extravascular migration of virally infected leucocytes and to treat CC asthma.

CC See also Q14651 and Q14830.
SQ Sequence 524 BP; 128 A; 130 C; 135 G; 131 T;

Query Match 68.4%; Score 277.2; DB 1; Length 524;
Best Local Similarity 81.4%; Pred. No. 3.1e-71;

Matches 337; Conservative 0; Mismatches 68; Indels 9; Gaps 1;

Qy 1,atgggttggaactgtatcatctctcttctgtgtaccacagctacagtggtgactccag 60
Db 34 ATGGGTGGAGCTGTATCATCTTCTTCTGTGTAGCAACAGCTACAGGTGTGACTCCAG 93

```

Qy 61 gtccagctggtgcaatctctggggtctgagtgagaagcctgtgagctcagtgaagtgctc 120
Db 94 GTCCAGCTGACACATCTGGGCTGTGAGTGGAGGCTCGGGGTCTGATGAAGATTCC 153
Qy 121 tgcagaagctccggttacacattcactgattatgctatcacagtggtgagacagctcct 180
Db 154 TGCAGAGGTTCGGGTACACATTCTATTATGCTATTACACTGGGTGAAGAGTCAAT 213
Qy 181 ggaagggcctcagtgagtgagtgatctaatatcttactatgataataacaactacaac 240
Db 214 GCAAGAGCTGTAGATGTGAGTTGAGTATTAGTCTCTCTGCTGAGACACAACTACAC 273
Qy 241 cagaagtttaaggcgaagccacaatgactgttagacaagtgcagcagccatattg 300
Db 274 CAGAGTTTAAAGGAGAGCCACAAATGACTGTTGACAAATCTCCAAACACCTATTGG 333
Qy 301 gaactagttcttgaagatcgaagatacgcgcgttattactgtgcaagcgcgccttg 360
Db 334 GAACATTGCCAGATTGACATCTGAGGATTGTGCCATCTATTACTGTGCAAGAGGGGATGG 393
Qy 361 -----tatatgactactcgtgggtcaaggtacacctgtcacgcctctca 405
Db 394 TTACTACTCTCTCTTGTGACTACTGCGGCCAAGGACACACTCTCAGACTCTCTCA 447

```

RESULT 3
Q05554
ID Q05554 standard; DNA: 446 BP.
AC Q05554;

DT 10-DEC-1990 (first entry)
DE Sequence encoding variable region of murine AHR 107 heavy chain.
KW Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss.
OS Mus sp.

FT Key Location/Qualifiers
FT cds 45..446
FT /*tag= a

FN EP-380068-A.
PN 01-AUG-1990.
PR 24-JAN-1990; 101351.
PR 24-JAN-1989; US-501216.
PR 04-DEC-1989; US-441702.
PA (MOLE-) MOLECULAR THERAPEU.
PI Zeller B;
DR WPI: 90-232892/31.
DR P-PSDB: R06250.

PT Expression vectors for producing chimeric monoclonal antibodies - PT which express human constant region and non-human variable region PS Disclosure; P; English.
CC MAb comprising mouse CH and CL constant regions which humans, CC variable regions may be used to create mouse/human hybrid Mabs, CC which have a longer serum half-life. Method can be used to produce CC Abs against Interleukin-2 receptor and tumour necrosis factor.
SQ Sequence 446 BP; 117 A; 110 C; 113 G; 106 T;

Query Match 67.2%; Score 272.2; DB 1; Length 446;
Best Local Similarity 81.2%; Pred. No. 8.1e-70;

Matches 329; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

Qy 1 atgggttggaactgtatcatctctcttctgtgtaccacagctacagtggtgactccag 60
Db 45 ATGGGCTGGAGCTGTATCATCTCTTCTGTGCGAGCAACAGCTACAAAGTGTGACTCCAG 104
Qy 61 gtccagctggtgcaatctctggggtctgagtgagaagcctgtgagctcagtgaagtgctc 120
Db 105 GTCCAGCTGACACATCTGGGCTGTGAGTGGAGGCTCGGGGTCTGATGAAGATTCC 164
Qy 121 tgcagaagctccggttacacattcactgattatgctatcacagtggtgagacagctcct 180
Db 165 TGCAGAGGTTCGGGTACACATTCTATTATGCTATTACACTGGGTGAAGAGTCAAT 224
Qy 181 ggaagggcctcagtgagtgagtgatctaatatcttactatgataataacaactacaac 240

ID	Accession	Gene	Protein	Length	Score	DB	Length	Score	DB
Db	225	GCAAGACTCTAGAGTGTGATTTAGTCTTACATGGTGTATACAGCTAAC	284	65.68	265.8	DB 1	1767	65.68	265.8
Qy	241	cagaagtttaaggcgaagcccaatgactgctgtatgacaagtcgacgacagctatag	300	65.68	265.8	DB 1	1767	65.68	265.8
Db	285	CCGAGGTTTAAGGGCAAGCCACATGATCTGTACAAATCCCTCCACACAGCTATATG	344	65.68	265.8	DB 1	1767	65.68	265.8
Qy	301	gaactagttcttctgaagtcgaagatacggccgtttattactgttgaagaagcgcttg	360	65.68	265.8	DB 1	1767	65.68	265.8
Db	345	GAACTTGCCAGATTGACATCTGGAAGATTCTTCATCTATTACTGTGGAAG--GGAAGC	401	65.68	265.8	DB 1	1767	65.68	265.8
Qy	361	tatatgactactggggtcgaagatgacccctgtcaccgctctcccta	405	65.68	265.8	DB 1	1767	65.68	265.8
Db	402	AACCTTGACTGACTGGGGCCAAAGCACCACCTGTACAGTCTCTCTA	446	65.68	265.8	DB 1	1767	65.68	265.8
RESULT	4								
ID	V61363	standard; cDNA to mRNA; 1767 BP.							
AC	V61363	18-JAN-1999 (first entry)							
DE	Anti-human Fas humanised antibody CH1 heavy chain HmuH cDNA.								
FW	Humanised antibody; Fas; CH1; monoclonal antibody; MA; apoptosis;								
KW	autoimmune disease; rheumatoid arthritis; therapy; human;								
OS	antibody engineering; ds.								
KS	Homo sapiens.								
OS	Synthetic.								
FT	Key	Location/Qualifiers							
FT	sig_peptide	1..57							
FT	/*tag= a	58..1764							
FT	mat_peptide	/*tag= b							
FT	EP-866131-A2.								
PN	23-SEP-1998.								
PD	20-MAR-1998; 302113.								
PF	21-MAR-1997; JP-067938.								
PA	(SANY) SANKYO CO LTD.								
PI	Haruyama H, Nakahara K, Serizawa N, Takahashi T,								
PI	Yonehara S;								
DR	WPI: 98-482965/42.								
DR	P-PSDB; W11880.								
PT	Production of anti-Fas protein humanised antibodies - for use in								
PT	inducing apoptosis on Fas expressing cells in the treatment of								
PT	autoimmune diseases, especially rheumatoid arthritis								
PS	Example 3; Page 103-105; 187BP; English.								
CC	This cDNA sequence codes for a humanised anti-Fas antibody CH1								
CC	heavy chain (see W11880), designated HmuH. HmuH is based on the								
CC	light chain (see W11888) of murine anti-human Fas monoclonal								
CC	antibody CH11. The humanised sequence was designed following								
CC	selection of donor residues from CH11 to be grafted onto acceptor								
CC	molecule 21.28/CL. 2 Light chain sequences (see W11880-81) have								
CC	been designed, and each can be used in combination with any of 4								
CC	light chain sequences (see W11876-79) to provide novel, claimed								
CC	humanised CH11 IgM antibodies that lack a J chain. These humanised								
CC	anti-human Fas antibodies are capable of inducing apoptosis in cells								
CC	expressing Fas (e.g. synovialocytes) and are useful in the treatment								
CC	of autoimmune disease and chronic rheumatoid arthritis. DNA								
CC	sequences encoding the humanised antibodies are claimed, as are								
CC	vectors such as pRimH5-1 including the HmuH nucleotide sequence,								
CC	and host cells such as Escherichia coli pRimH5-1 (FERM BP-5865).								
CO	Sequence 1767 BP; 384 A; 368 C; 485 G; 350 T;								
Query Match	Best Local Similarity	65.68; Score 265.8; DB 1; Length 1767;							
Matches	318; Conservative	0; Mismatches 87; Indels 0; Gaps							
Qy	1	atggagttggaacgtatcatcttcttctctgtgtaccacagctacaggtgtgactccag	60	65.68	265.8	DB 1	1767	65.68	265.8
Db	1	ATGGAGATGAGACTGAGACTTCTCTCTCTCTCTGTCAGGAACCTGACGACGTCACCTGAG	60	65.68	265.8	DB 1	1767	65.68	265.8
Qy	61	gtcagcgtggtgaggtcttggggcgtgaaggtgaagaagcctggagactgaagaggtctc	120	65.68	265.8	DB 1	1767	65.68	265.8

Db	61	GTGCAGCTTGAGAGCTCTGGGCGCTAGGTGAAGAAGCGCTGGGGCGCTCAGTGAAGAAGTTTCC	12
Qy	121	tgcagaagcttcggcgtaacacattcactgattatgctatcacagtgggtgagacgctct	18
Db	121	TGCAGAAGCTTCTGGAGATGACCTTCCTACTACATATATATGATTTGGGTGGCGCCAGGCCCC	18
Qy	181	ggccagagcgctcgtagtgagttggagttatattatattaccatgatatacaaacatcaac	24
Db	181	GGCCAAAGAGCTCGAATAGGATGGGATATATTTATCTTACATATGATGTGTAAGTGGCTTCAAC	24
Qy	241	cagaagtttaagggcacaagcccaatagactgtagacaagtcgacgagcacaagctatag	30
Db	241	CAGAAGTTCAAGAGCAAGGCCACATATGACTGTTACAAATTTCCGAGACAGAGCTTACAG	30
Qy	301	gaactagttcttcttgagatctgagatacgcgcttattactgtgcaagagcgcgctg	36
Db	301	GACCTAGAGCAGCGCTGAGATCTGAAACACAGGCTGTATTTACTGTGTCGAGAAAGTTACTAT	36
Qy	361	tatatgactactgggtgtaaggtacccctgtcacccgtcccca	405
Db	361	GCTATGAGCTACTGGGGCGCAGGAGCACTGGTGACCGCTTCTCA	405
RESULT	5		
ID	V61364	standard; cDNA to mRNA; 1768 BP.	
AC	V61364;		
DE	18-JAN-1999	(first entry)	
DT	Anti-human Fas humanised antibody CH11 heavy chain HmM cDNA.		
KW	Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;		
KW	autoimmune disease; rheumatoid arthritis; therapy; human;		
OS	antibody engineering; ds.		
OS	Homo sapiens.		
FT	Synthetic.		
FT	Key	Location/Qualifiers	
FT	CDS	1..1767	
FT		/*tag= a	
FT	sig_peptide	1..57	
FT		/*tag= b	
FT	mat_peptide	58..1764	
FT		/*tag= c	
PN	RP-866131-A2.		
PD	23-SEP-1998.		
PE	20-MAR-1998; 302113.		
PR	21-MAR-1997; JP-067938.		
PA	(SANY) SANKYO CO LTD.		
PI	Haruyama H, Nakahara K, Serizawa N, Takahashi T,		
PI	Yonemura S.		
DR	WPI; 98-482965/42.		
DR	P-PDSB; W71881.		
PT	Induction of anti-Fas protein humanised antibodies - for use in		
PT	inducing apoptosis on Fas expressing cells in the treatment of		
PT	autoimmune diseases, especially Rheumatoid arthritis		
PS	Example 3; Page 108-110; 187pp. English.		
CC	This cDNA sequence codes for a humanised anti-Fas antibody CH11		
CC	heavy chain (see W71881), designated HmM. HmM is based on the		
CC	light chain (see W71888) of murine anti-human Fas monoclonal		
CC	antibody CH11. The humanised sequence was designed following		
CC	selection of donor residues from CH11 to be grafted onto acceptor		
CC	molecule 21.28/Cl. 2 light chain sequences (see W71880-81) have		
CC	been designed, and each can be used in combination with any of 4		
CC	light chain sequences (see W71876-79) to provide novel, claimed		
CC	humanised CH11 IgM antibodies that lack a J chain. These humanised		
CC	anti-human Fas antibodies are capable of inducing apoptosis in cells		
CC	expressing Fas (e.g. synoviocytes) and are useful in the treatment		
CC	of autoimmune disease and chronic rheumatoid arthritis. DNA		
CC	sequences encoding the humanised antibodies are claimed, as are		
CC	vectors such as pHmuM1-1 including the HmM nucleotide sequence,		
CC	and host cells such as Escherichia coli pHmuM1-1 (FERM BP-5864).		
CC	Sequence 1768 BP; 387 A; 564 C; 485 G; 332 T;		
Query Match	65.6%; Score 265.8; DB 1; Length 1768;		

Best Local Similarity 78.5%; Pred. No. 8.8e-68;
Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

```

OY 1 atgggttggaactgtatcatctctcttcttggttacacagcagcaggtgtgactccag 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ATGGGATGGAGTGGATCTTCTCTCTCCCTGTCAGAGTGCAGAGCCTCCACTCTGAG 60
OY 61 gccacgtctgtcaactctgagctgagctgaaagccctggagcagcagtgaaagtgtcc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 GCGCAGCTTGTGCAGCTGCGGCTGAGTGAGAGACCTGGGGCCCTCATGAGGTTTCC 120
OY 121 tgcnaagcttcgcgttacacattcagttatgtctatacagtgagtgagaggtcct 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 TCCAGAGCTTCTGATACCTCTTCACTGACTATTAATATCATTTGGGTGAGAGGCCCAT 180
OY 181 ggcacggcctcagtgatgttgagttatataatattactatgataataacaactacaac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 GGAAGAAGCCTGGAATGAGTGGATATATTATCTTACAAATGTTGTTACTGGCTAACAC 240
OY 241 cagaagtttaaggcagaagccacaatgactgtagacaagctgcagcagcagcctatag 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 CAGAGTTTCAAGACAGCAGCCACATTGACTGTTGACAAATCCGCGAGCAGACGCTTACAG 300
OY 301 gaactagttctttagatctgagatcagcagcagcgtttattactgtgcaagaagcgctcg 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 GAGCTGAGCAGCCTGAGATCTGAGACAGCAGCGCTGTGTATTACTGTGCGAAGATTACTAT 360
OY 361 tatatgactactggtggtcaaggtacacctgtgcacggttactca 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 361 GCTATGACTACTGTGGGCGAGGACCCGTGTACCGTCTCCCA 405

```

RESULT 6

T42717

ID T42717 standard; DNA: 424 BP.

AC T42717.

DT 04-FEB-1997 (first entry)

DE Humk3 VH coding sequence.

KW Humk3 VH: BA46 antigen; human; milk fat globule; HMFG; lactation;

KW fat globule membrane; murine; mammary; epithelial cell; breast cancer;

KW breast membrane glycoprotein; therapy; immunotherapy; ss.

KM Synthetic.

OS Synthetic.

FH Key Location/Qualifiers

FT cds 11. 418

FT /*tag= a /product= Humk3 VH (BR-M version)

FN MO9608565-A2.

PD 21-MAR-1996.

PF 14-SEP-1995; U11683.

PR 16-SEP-1994; US-107868.

PR 07-JUN-1995; US-487598.

PA (CANC-) CANCER RES FUND CONTRA COSTA.

PI Certant R1, Do Couto FUR, Peterson JA;

DR P-PSDB; W06442.

DR WPI; 96-179941/18.

PT Recombinant MC3 antibody which binds BA46 antigen of HMFG -

PT comprises a modified heavy or light chain variable region, useful in

PT the diagnosis and therapy of breast cancer

PS Claim 13; Fig 18; 91pp; English.

CC This sequence represents the coding sequence for the variable heavy (VH)

CC chain of the humanised murine antibody Humk3 VH. The MC3 VH sequence was

CC humanised using the buried residue modification technique, where

CC important non-human framework residues are unaffected. The MC3 antibody

CC binds to the BA46 antigen of the human milk fat globule (HMFG). The milk

CC fat globule membrane is derived from the apical surface of the mammalian

CC epithelial cell during lactation, and therefore is a source for breast

CC membrane glycoproteins. The antibody can be used in an in vitro method

CC to detect a HMFG antigen (or antigen fragment), and to diagnose the

CC presence of the antigen in a subject. The antibody can also be used to

CC deliver an agent to a target (within a subjects body), containing a HMFG

CC antigen. The antibodies can also be used for diagnosis, prognosis, and

CC therapeutic applications of breast cancer. As the humanised antibodies

CC retain their high affinity binding to the antigen, they are useful for
CC immunodiagnostic and immunotherapeutic applications in humans.
SQ Sequence 424 BP; 106 A; 102 C; 112 G; 104 T;

Query Match 62.8%; Score 254.4; DB 1; Length 424;
Best Local Similarity 78.2%; Pred. No. 1.1e-64;
Matches 319; Conservative 0; Mismatches 86; Indels 3; Gaps 1;

```

OY 1 atgggttggaactgtatcatctctcttcttggttacacagcagcaggtgtgactccag 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 11 ATGAATGAGCTGGATGATTTCTTCTCTCCCTGTCAGAGTGCAGAGTGTCTCAGTGG 70
OY 61 gccacgtctgtcaactctgagctgagctgaaagccctggagcagcagtgaaagtgtcc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 GCGCAGCTTGTGCAGCTGCGGCTGAGTGAGAGACCTGGGGCCCTCATGAGGTTTCC 130
OY 121 tgcnaagcttcgcgttacacattcagttatgtctatacagtgagtgagaggtcct 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 TCCAGAGCTTCTGATACCTCTTCACTGACTATTAATATCATTTGGGTGAGAGGCCCAT 190
OY 181 ggcacggcctcagtgatgttgagttatataatattactatgataataacaactacaac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 GGAATGAACCTTGAATGAGTGGATATATTATCTTACAAATGTTGTTACTGTCTAACAC 250
OY 241 cagaagtttaaggcagaagccacaatgactgtagacaagctgcagcagcagcctatag 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 251 CAGAGTTTCAAGACAGCAGCCACATTGACTGTTGACAAATCCGCGAGCAGACGCTTACAG 310
OY 301 gaactagttctttagatctgagatcagcagcagcgtttattactgtgcaagaagcgctcg 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 311 GAGCTGAGCAGCCTGAGATCTGAGACAGCAGCGCTGTGTATTACTGTGCGAAGATTACTAT 370
OY 361 ta---tatgactactggtggtcaaggtacacctgtgcacggttactca 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 371 TATACTATGACTATTTGGGCTCAAGGAACCCGTGTACCGTCTCCCA 418

```

RESULT 7

ID 066702

AC 066702 standard; CDNA: 451 BP.

DT 16-NOV-1994 (first entry)

DE DREG-200 Humanized antibody heavy chain variable region.

KW DREG-200; L-selectin; LECAM-1; Mel-14; LAM-1;

KW humanized antibody; immunoglobulin; Ig; IgG1; IgG4;

KW complementarity determining region; CDR; monoclonal antibody; Mab;

KW framework; light chain; heavy chain; variable domain;

KW monoclonal antibody; acceptor antibody Eu; transgenic animal; ss.

OS Mus sp.; Homo sapiens

FH Key Location/Qualifiers

FT cds 12. 434

FT /*tag= a

FT signal_peptide 12. 68

FT /*tag= b

FT mat_peptide 69. 431

FT /*tag= c

FN MO9412215-A.

PD 09-JUN-1994.

PF 30-NOV-1993; U11612.

PR 01-DEC-1992; US-983946.

PA (PROT-) PROTEIN DESIGN LABS INC.

PI Co MS;

DR WPI; 94-199974/24.

DR P-PSDB; R55556.

PT New humanised antibody specific for L-selectin - with murine CDR

PT and human framework regions, inhibits binding of neutrophils to

PT endothelial cells and useful for treating or preventing

PT inflammation

PS Disclosure; Fig. 3B; 60pp; English.

CC An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs

CC corresponding to those of mouse Mab DREG-200 and heavy and light

CC chain variable region frameworks of the human acceptor antibody Eu.

Db 141 TGCAGGCTTGTGGCTACACCTTCACAGCTACTGATGACGGTGAATAACAGCCCT 200
 Qy 181 ggaacagggccctcgatggtggtggtatcttactatgatacaactaac 240
 Db 201 GGACAGGCGCTTGAGTGGATGGAGATTGATCTTCTGTACTACTATACCTAACAT 260
 Qy 241 cagaagtttaagggcaaggaacatgactgtagcaagtagagacagacagctatg 300
 Db 261 CAAAGTTCAAGGCGCAAGGCCACATGTACTATACACATCCATACGACGCTACATG 320
 Qy 301 gaactagttcttgatgactgtaggatacggcgcttattactgtagaaga----- 351
 Db 321 GAGCTCAGACGCTGAGATCTGAGACACGCGGCTATTACTGTGCAAGAAATAGGAC 380
 Qy 352 -----gcggcctggtatattgactactggtggtcaaggtaccctgtccacgctctca 405
 Db 381 TATAGTAACAACCTGTACTGTGATGTGGGGGCAAGGAGCCGTGTCACGCTCTCA 440

RESULT 9
 ID V70104 standard: cDNA to mRNA: 457 BP.
 AC V70104;
 DE 15-MAR-1999 (first entry)
 KW Anti-Fas humanised antibody HFE7A heavy chain variable region cDNA.
 KW HFE7A: monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; ds.
 OS Homo sapiens.
 FH Key
 FT CDS
 FT 21..458 Location/Qualifiers
 FT /tag- a
 FT 21..77
 FT /tag- b
 FT 78..455
 FT mat_peptide
 FT /tag- c
 PN A09859701-A.
 PD 08-OCT-1998.
 PE 30-MAR-1998: 059701.
 PR 08-OCT-1997: JP-276064.
 PR 01-APR-1997: JP-082953.
 PR 25-JUN-1997: JP-169088.
 PA (SANY) SANKYO CO LTD.
 PI Akiro S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I,
 PI Masahiko O, Nobuhisa S, Shin Y, Tohru T;
 DR WPI: 98-543440/47.
 DR P-PSDB: W83038.
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 PS Example 3; Page 206-207; 292pp; English.
 CC This nucleotide sequence codes for the VD type humanised heavy
 CC chain variable region (see W83038) of murine anti-human Fas
 CC monoclonal antibody HFE7A. It was utilised in the construction
 CC of a claimed humanised HFE7A heavy chain (see V70079). The
 CC invention provides methods for producing humanised antibodies by
 CC culturing host cells. Humanised versions of HFE7A (see W83031-37)
 CC are capable of inducing apoptosis in abnormal cells expressing Fas,
 CC and of inhibiting Fas-induced apoptosis in normal cells. Humanised
 CC antibodies are used to evaluate, in animal models, treatments of
 CC diseases that involve Fas/Fas ligand interactions, and also to
 CC treat such diseases, including autoimmune disease (e.g. systemic
 CC lupus erythematosus, Hashimoto's disease, graft versus host disease,

CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
 CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
 CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
 CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 SQ Sequence 457 BP; 113 A; 117 C; 126 G; 101 T;

Query Match 61.4%; Score 248.8; DB 1; Length 457;
 Best Local Similarity 76.9%; Pred. No. 4.7e-63;
 Matches 323; Conservative 0; Mismatches 82; Indels 15; Gaps 1;

Qy 1 atggtttgaactgtatcatcttcttctggtaccagagcttgcacccag 60
 Db 21 ATGGGATGGAGCTGTGATCCCTTCTTGAGAACAGCTACAGTCTCCACTGAG 80
 Qy 61 gtccagctggtgaactgtggtggtggtggaagagcctggagctcagttgctc 120
 Db 81 GTCCAACTGCTGCGTGTGGGCTGAGTCAAGACCTGGGCTTCACTGAAGGTGTC 140
 Qy 121 tgcgaagcttcggctcacacatcactgatactgtatatacagtgagagagctcct 180
 Db 141 TGCAGGCTTGTGGCTACACCTTCACAGCTACTGATGACAGGCTTAACAGGCCCT 200
 Qy 181 ggaacagggcctcgatggtggtggtatcttactatgatacaactaac 240
 Db 201 GGACAGGCGCTTGAGTGGATGGAGATTGATCTTCTGTACTACTATACCTAACAT 260
 Qy 241 cagaagtttaagggcaaggaacatgactgtagcaagtagagacagacagctatg 300
 Db 261 CAAAGTTCAAGGCGCAAGGCCACATGTACTATACACATCCATACGACGCTACATG 320
 Qy 301 gaactagttcttgatgactgtaggatacggcgcttattactgtagaaga----- 351
 Db 321 GAGCTCAGACGCTGAGATCTGAGACACGCGGCTATTACTGTGCAAGAAATAGGAC 380
 Qy 352 -----gcggcctggtatattgactactggtggtcaaggtaccctgtccacgctctca 405
 Db 381 TATAGTAACAACCTGTACTGTGATGTGGGGGCAAGGAGCCGTGTCACGCTCTCA 440

RESULT 10
 ID V70079 standard: DNA: 2077 BP.
 AC V70079;
 DE 15-MAR-1999 (first entry)
 KW Anti-Fas humanised antibody HFE7A heavy chain DNA.
 KW HFE7A: monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; ds.
 OS Homo sapiens.
 FH Key
 FT CDS
 FT 27..2042 Location/Qualifiers
 FT /tag- a
 FT /note- "contains introns"
 FT 28..83
 FT /tag- b
 FT 1..741
 FT /tag- c
 FT /number- 1
 FT /codon_start- 27
 FT Intron 742..1132

Query Match	Best Local Similarity	Matches 323: Conservative	Score 61.4%	DB 1: 248.8	Length 2077:
1 atgggttggaatgatactatcctctcttcgtggtacacagctacaggtgtgctccag	76.9%	0: Mismatches 82: Indels 15: Gaps 1			
27 ATGGATGAGACTGTRATCTCTCTCTTCTTGTAAGCAACAGCTACAGTGTCCACTTCAG					
61 gtccagctgtgtcagctctgtgggtcgaagtgaagaagcctgtggagctcagtgaaagtgtcc					
87 GTCACAACTGTCAGACTGGGGCTGAGGCAAGAAAGCCTGTCAAGTGAAGGTCTC					
121 tgcgaagcttcgcgtacacatcctgattatgctatcaggtgggtgtgacaggtcct					

ID	Accession	Score	Length	Indels	Gaps
Db	147	TCGACAGGCTTCTGGCTACACCTTACACACGCTACTGAGTCAGTGGGTAAACAGGCCCT	206		
Qy	181	ggacagggcgctcagatggaattggaattataattactatgatataatacaactacaac	240		
Db	207	GGACAGAGGCTTGAAGTGATGGAGAGANTGATTCCTTCGTGATAGCATATCTACTCAAT	266		
Qy	241	cagaagttaaggagcgaagccacaatgactgtagacaagtcgacgacagccatata	300		
Db	267	CAAAAGTTCAAGGAGGAGGAGCCACATTTGATGTAGACACATCCGCTAGCAGCCTACATG	326		
Qy	301	gaactagttctttagatctagatagatagagcgcttattactatgycaga-----	351		
Db	327	GAGCTCAGAGCCTTGAGATCTTAGGACACAGGGGCTATTACTGTCTCAAGAAATAGGAC	386		
Qy	352	-----gcgacctgtatatagactactgaggtcgaagtagaccccttcacgctcctca	405		
Db	387	TATAGTAACAACTGGTACTGTGATGATGCTGGGCGAAGGAGCCTTGCTACCGTCTCTCA	446		
RESULT	11				
ID	V33947	standard; cDNA; 405 BP.			
AC	V33947:				
DT	15-FEB-1999	(first entry)			
DE	Anti-CD3 antibody heavy chain cDNA.				
KW	Fanconi anaemia complementation group C; FAC; apoptosis;				
KW	haematopoiesis; bone marrow; chemotherapy; gene therapy;				
OS	CD3; antibody; ds.				
OS	Class - Mammalia.				
PN	WO9851792-A1.				
PD	19-NOV-1998.				
PF	15-MAY-1998; 009975.				
PR	15-MAY-1997; US-046546.				
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.				
PI	Yousoufian H;				
DR	WPI: 99-009774/01.				
DR	P-PDB: W68546.				
PT	New conjugate of Fanconi anaemia molecule and peptide selective for				
PT	haematopoietic precursor cells - inhibits apoptosis of these cells,				
PT	for treating Fanconi anaemia and patients undergoing high-dose				
PT	chemotherapy for cancer				
PS	Example 1; Page 50-51; 72pp; English.				
CC	This cDNA clone comprises a coding region for the heavy chain (see				
CC	W68546) of the M195 anti-CD3 antibody. This antibody selectively				
CC	binds to surface of haematopoietic progenitor cells (HPC) and is				
CC	transported into the cells by endocytosis. The invention provides				
CC	conjugates of human Fanconi anaemia complementation group C (FAC)				
CC	protein (see W68546) and anti-CD3 antibody (preferably a single				
CC	chain antibody). A nucleic acid encoding the heavy chain can be				
CC	ligated with vector pED6 and with FAC cDNA (see V33945) to provide				
CC	a fusion protein. Alternatively, nucleic acids encoding the heavy				
CC	and light chains (see V33948) of M195 are ligated into a bicistronic				
CC	vector; antibody molecule is isolated from transfected cells; and				
CC	chemically crosslinked to FAC protein (see W68546) to form a				
CC	conjugate. The conjugate or fusion protein, or a nucleic acid				
CC	encoding it, can be used to deliver FAC to an HPC, specifically to				
CC	inhibit apoptosis, particularly in patients exposed to high doses				
CC	of chemotherapy for treatment of non-myeloid cancers, also to treat				
CC	Fanconi anaemia (by complementation of the genetic defect).				
CC	Treatment of HPC is done in vitro, ex vivo (e.g. for recombinant				
CC	production of conjugate in cell cultures) or in vivo. Treatment				
CC	with FAC may eliminate the need for extensive bone marrow				
CC	transplants to restore haematopoiesis after chemotherapy.				
CC	Sequence 405 BP; 101 A; 106 C; 105 G; 93 T;				
Qy	Query Match	60.5%;	Score 245;	DB 1;	Length 405;
Qy	Best Local Similarity	75.3%;	Pred. NO. 5,7e-62;		
Qy	Matches 305; Conservative	0;	Mismatches 100;	Indels	0;
Qy	1 atggattggaactatcatctcttcttggttacacagctacaggtgtgactccag	60			
Qy	1 atggatggagctgattcttctctccctcgtcaggaacacgagggcctccacttgag	60			

Oy	61	gttcaagctcggcgagcagctctcggggcgctgaagaggaagcctcggagagctcaagctgaagagctctc	120
Db	61	gtccacgcttcacgacgactcagacaccttcgactcgttgaacctggggccttcagctgaagatattcc	120
Oy	121	tgcgaagcttcgcgcgtacacacattcaactgattatgctatacaagtggtgtagacagcgtcctc	180
Db	121	tgcgaagcgtttgtgatatacattatcagactacacacatgacacgtgggaagcagagccat	180
Oy	181	ggacagggccctcgcgctcgatctgagctattataattcactcagtataatacaactcaac	240
Db	181	ggaaagagcccttgatggtgatattggatatattatcttaccatagctggtacttggtctaac	240
Oy	241	cagaagctttaaaggccaagggccaacaatgactcgtatagaacaagtgcagagcagacacctatag	300
Db	241	cagaaagttcaagagacacaaagccacattgtatgactgtatgacaaattctccacaaacagccttaatg	300
Oy	301	gaactttagttcttcggagatctcgagatagacagcgcttattactctgcaagagcggccttg	360
Db	301	gacgcgcgcacactgcacatcttgagagactctcagctattattactgtgcamaagggcgccc	360
Oy	361	tatatagactactcgggtgccaagctacccctgtctacgctctcccta	405
Db	361	gctataggactactggggctcaagaaacctcactacccgtctccta	405

RESULT 12

V37264

ID V37264 standard; cDNA; 405 BP.

AC V37264;

DT 10-SEP-1998 (first entry)

DE cDNA encoding a variable region of an anti-Fas antibody heavy chain.

KW Variable region; heavy chain; anti-Fas antibody; human; mouse;

KW Immunoglobulin G; IgG; light chain; treatment; diagnosis;

KW autoimmune disease; ss.

OS Mus sp.

PN J10165178-A.

PD 23-JUN-1998.

PF 01-JUL-1997; 191769.

PF 09-OCT-1996; JP-268737.

PR 02-JUL-1996; JP-172228.

PA (IGAK-) IGAKU SEIBUSUGAKU KENKYUSHO KK.

DR WPI: 98-406105/35.

PT DNA encoding, e.g. variable region of anti-Fas antibody - useful

PT for, e.g. diagnosis and treatment of auto-immune diseases

PS Claim 2; Page 12; 16pp; Japanese.

CC The present sequence encodes a variable region of the heavy chain of an

CC anti-Fas antibody. The constant region of the heavy chain is derived

CC from human immunoglobulin G (IgG). The anti-Fas antibody can be used

CC for the treatment and diagnosis of autoimmune diseases.

SO Sequence 405 BP; 103 A; 102 C; 98 T;

Query Match	60.1%;	Score 243.4;	DB 1;	Length 405;
Best Local Similarity	75.1%;	Pred. No. 1.7e-61;		
Matches 304; Conservative	0;	Mismatches 101;	Indels 0;	Gaps 0;

[illegible]

Qy	241	cagaagtttaagggccaagggccacacatgactgctgtgacaaagtcgcagacagacaaagcctatag	3000
Db	241	CAGAAGTTCAGAGACCAAGGGCCACATTGACTGTGCAATTCCTCCACACAAAGCCTACATG	3000
Qy	301	gaacttagttctttagagatcgtgaagatagcgctttatctactgtgcaagagcgccttg	3600
Db	301	GAGCTCCCGACCTGACATCTGAGAGACTCTGCACATCTATTACTGTGCAAGAGTTACTAT	3600
Qy	361	tatatgactactggggtcgaagtcacactgttcacgcgttcctcca	405
Db	361	GCTATGACTACTGGGGGTCAAGGAACCTCAACCTACCTCTCTCTCA	405

RESULT	13
ID	T88869
AC	T88869 standard; DNA; 1773 BP.
DJ	T88869;
DT	15-APR-1998 (first entry)
DE	H chain subunit of Fas specific antibody coding sequence.
KW	Fas: antibody; human; immunoglobulin; variable region; rheumatism; autoimmune disease; rheumatoid arthritis; therapy; CDR; heavy chain; complementarily determining region; ss.
OS	Mus musculus.
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1773
FT	/tag= a
FT	1..57
FT	/tag= b
FT	58..1770
FT	/tag= c
PM	EP-799891-A1.
PD	08-OCT-1997.
PF	27-MAR-1997; 302415.
PR	01-APR-1996; JP-078570.
PA	(SANY) SANKYO CO LTD.
PI	Ichikawa K, Nakahara K, Serizawa N, Yonehara S; WPT: 97-482673/45.
DR	P-PDBI; W31751.
PT	Anti-Fas recombinant antibodies - useful for treating auto-immune diseases, especially rheumatoid arthritis
PS	Claim 18; Page 29-31; 72pp; English.
CC	This sequence represents the coding sequence for the heavy chain of the protein of the invention. The protein is a recombinant immunoglobulin (Ig) variable region which enables the protein to recognize and specifically bind to an antigen, preferably human Fas, and has substantially no more immunogenicity in a human patient than a human antibody. The proteins are useful for treating autoimmune diseases, especially rheumatism (rheumatoid arthritis). (A) is based on a murine monoclonal antibody. As the protein lacks the constant region, it has substantially no more immunogenicity in the human patient than a human antibody.
Sequence	1773 BP; 455 A; 512 C; 416 G; 390 T;

Query Match 60.1%; Score 243.4; DB 1; Length 1773;
Best Local Similarity 75.1%; Pred. No. 2.6e-61;
Matches 304; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 atgggttggaaactgtatatcatcttcttcttcgtgtaccaaagtaaggtgycatcccaag 60

Db 1 ATGGATGAGACATGTATCTTCTCTCTCCTGTCAGAGAACTGACGCGTCACCTTGAG 60

QY 61 gtccagcctcggtgfcagttctcggggcctgaggtgaagaagcctggggagctcaagtgaaagtctc 120

Db 61 GTCCAGCCTTCAGACAGTCAGGAGCTGAGCTGGTGAACCTGGGGCCTCAGTGAAATATCC 120

QY 121 tgcgaagcttcgcgcgttaacaattcaactgattatgctctatacagtggtggtgagaacagcgtcct 180

Db 121 TGCAGAGCTTCGTGGATACATCATTACATGCAATCAACAACATGCACCTGGTGGAACAGGCAT 180

QY 181 ggacagggcctcagatgtgatttggagttataatattcaacttgatataacaactaacac 240

Oy 181 cgaagggccgcagatggtatgggtatataatcttaccatgataaacaactcaac 240
 Db 227 gacacagcccttgatgatgatggaatgattatccttaattgctgatactactacaa 286
 Oy 241 cagaagttiaaggycaaagccacaaatgactgtagacaagtcgaagacacagctaatg 300
 Db 287 gagaaattcaagagacaaagccacactgactgtatagcaaaatctctcacacagcctatc 346
 Oy 301 gaacttagttccttgagatctcgagatgatacggcgcttattactgtgcaagag----- 352
 Db 347 caatccacacacctgcacactctgaaagacactccggctctattactgtgcamaagacagctca 406
 Oy 353 -----cgagcgtgatatgactgacttgggttcaagtgtaacctttcacagctctctca 405
 Db 407 gcctacgactatgctatgactatgactatggggtcamaagaaactcactgacacccgtctctca 463

Search completed: August 27, 2000, 06:25:32
Job time: 1929 sec

Db	61	GOGLEWIGNTYPPSSSTNNNEKRSKATLTPTSSSTAYVMOLSSLTSDSAVYYCARLWG	120
OY	61	GOGLEWIGVNTINYDNTNNNOKFKGNATVTYVKSTSTAMELSSLRSDTAVYYCARAA	119
Db	121	RYYAMDYWGOGTSVTSS	138
OY	120	WY--MDYWGOGTLVTYSS	135
RESULT	4		
ENTRY		A30577	#type fragment
TITLE		Ig heavy chain precursor V region (MR110) - mouse (fragment)	
ORGANISM		#formal_name Mus musculus #common_name house mouse	
DATE		04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996	
ACCESSIONS		A30577	
REFERENCE		A30577	
#authors		Kotler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theofilopoulos, A.N.	
#journal		J. Exp. Med. (1985) 161:805-815	
#title		Genetic elements used for a murine lupus anti-DNA autoantibody are closely related to those for antibodies to exogenous antigens.	
#cross-references		MOID:85159423	
#accession		A30577	
#status		preliminary	
#molecule_type		mRNA	
#residues		1-135 ##label KOR	
#cross-references		GB:M37621	
CLASSIFICATION		#superfamily Immunoglobulin V region; Immunoglobulin heterotetramer; Immunoglobulin	
FEATURE			
KEYWORDS			
34-117		#domain immunoglobulin homology #label IMM	
SUMMARY		#length 135 #checksum 8166	
Query Match		70.6%; Score 705; DB 2; Length 135;	
Best local similarity		71.9%; Pred. No. 6,80e-106;	
Matches		97; Conservative 18; Mismatches 20; Indels 0; Gaps 0;	
Db	1	MGMWCIIFLYAATGVHSOVLQDGGALVYPGASVYKSCASCAGYTTSTYIMNWKRP	60
OY	1	MGMWCIIFLYATVATGVHSOVLQSGALVYKPGSSVYKSCASGYTTTDAIQWKRAP	60
Db	61	GOGLEWIGNTYPPSSSTNNNEKRSKATLTPTSSSTAYVMOLSSLTSDSAVYYCARLWG	120
OY	61	GOGLEWIGVNTINYDNTNNNOKFKGNATVTYVKSTSTAMELSSLRSDTAVYYCARAAW	120
Db	121	GFAVWGOGTLVTYSA	135
OY	121	YMDYWGOGTLVTYSS	135
RESULT	5		
ENTRY		JL0076	#type fragment
TITLE		Ig heavy chain precursor V region (anti-phenylloxazalone, 18C10) - mouse (fragment)	
ORGANISM		#formal_name Mus musculus #common_name house mouse	
DATE		31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999	
ACCESSIONS		JL0076	
REFERENCE		JL0076	
#authors		Kaartinen, M.; Rocca-Serra, J.; Maekela, O.	
#journal		Mol. Immunol. (1988) 25:859-865	
#title		Combinatorial association of V genes: one VH gene codes for three non-cross-reactive monoclonal antibodies each specific for a different antigen (phloxazalone, NP or GAT).	
#cross-references		MOID:89096973	
#accession		JL0076	
#molecule_type		mRNA	
#residues		1-141 ##label KAA	
#cross-references		GB:M27788; NID:g195651; PIDN:AAA8441.1; PID:g195852	
CLASSIFICATION		#superfamily Immunoglobulin V region; Immunoglobulin homology	


```

DATE 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
18-Oct-1996

ACCESSIONS A27472
REFERENCE A27472
#authors Litv, A.Y.; Mack, P.W.; Champion, C.I.; Robinson, R.R.
#journal Gene (1987) 54:33-40
#title Expression of mouse:human immunoglobulin heavy-chain im-
Lymphoid cells.
#cross-references M01D:8727450
#accession A27472
##molecule_type mRNA
##residues 1-131 ##label LIT
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-19 #domain signal sequence #status predicted #label SIG\
5-54 #region complementarity-determining 1\
20-131 #product Ig heavy chain V region 1E9 #status predicted
#label MAT\
34-117 #domain immunoglobulin homology #label IMM\
69-88 #region complementarity-determining 2\
118-125 #region complementarity-determining 3
SUMMARY #length 131 #checksum 1501

Query Match 68.4%; Score 683; DB 2; Length 131;
Best Local Similarity 70.5%; Pred. No. 8,92e-102;
Matches 93; Conservative 18; Mismatches 18; Indels 3; Gaps 3;

Db 1 MGWSYILFLVATRAVDHSGVQLQDQGAELVPGASVYKSCASGYTFTSYMMHWKORP 60
OY 1 MGWNCILFFLVATRAVGHSGVQLQVSGAELVPGKSGVSKCASGYTFTDAIQWROAP 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 GGGHDWIGELINPGRNTEKRSKATLTVPKSSSTAYMAQSSITSDSAVYICASYD 120
OY 61 GGGLEWIGVNTIYDNTNNQKRGKATVTVKSSSTAYMAELSSRSDEITAVYICAR-A- 118
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 121 DWF-AVWGSGTL 131
OY 119 AWYMDWVGQCTL 130
|:|||||

RESULT 8
ENTRY GZMS43 #type complete
TITLE Ig heavy chain precursor V region (S43) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
22-Jun-1999

ACCESSIONS A02038
REFERENCE A90809
#authors Botchwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.;
Rajewsky, K.; Baltimore, D.
#journal Cell (1981) 24:625-637
#title Heavy chain variable region contribution to the NP(b) family
of antibodies: somatic mutation evident in a gamma2a
variable region.
#cross-references M01D:81234548
#accession A02038
##molecule_type mRNA
##residues 1-137 ##label BOT
##cross-references GB:J00539; NID:J195118; PIDN:AAA38172.1; PID:G195119
##note the gamma-2a chain mRNA was cloned from a hybridoma
making antibodies to the harten
(4-hydroxy-3-nitrophenyl)acetyl (NPb antibodies)
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-19 #domain signal sequence #status predicted #label SIG\
20-137 #product Ig heavy chain V region (S43) #status predicted
#label MAT\
34-117 #domain immunoglobulin homology #label IMM\
118-122 #region D segment (JH2)
123-137 #region J segment (JH2)
SUMMARY #length 137 #molecular-weight 15200 #checksum 474

```

Query Match 68.4%; Score 683; DB 1; Length 137;
 Best Local Similarity 67.2%; Pred. No. 8.92e-102;
 Matches 92; Conservative 23; Mismatches 20; Indels 2; Gaps 1;

Db 1 MGNCMIFLFLATATGVSQVLOOQPGAEVYKPCASVYKSLCKSGYFTDTLHMVNR 60
 1 MGNCMIFLFLATATGVSQVLOOQPGAEVYKPCASVYKSLCKSGYFTDTLHMVNR 60
 1 MGNCMIFLFLATATGVSQVLOOQPGAEVYKPCASVYKSLCKSGYFTDTLHMVNR 60

QY 61 GQGLEWIGVINYIDNTNMYNKKFKATMTVDKSTAYMELSLRSDTAIVYCAR--A 118
 61 GQGLEWIGVINYIDNTNMYNKKFKATMTVDKSTAYMELSLRSDTAIVYCAR--A 118

Db 121 GRPYDWGOGTTLTVSS 137
 121 GRPYDWGOGTTLTVSS 137
 119 AWYMDYWGOGTTLTVSS 135

RESULT 9
 ENTRY A27609 #type complete
 TITLE Ig heavy chain precursor V region (129) - mouse
 ORGANISM Mus musculus #common_name house mouse
 DATE 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999

ACCESSIONS A27609
 REFERENCE A27609
 #authors Klein, D.; Nietupski, J.; Strlin, S.; Stavnezer, J.
 #journal J. Immunol. (1988) 140:1676-1684
 #title I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch.
 #cross-references M01D:88154467
 #accession A27609
 #molecule_type DNA
 #residues 1-139 #label KLE
 #cross-references EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g953592

GENETICS 16/1
 #introns
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 FEATURE 1-19
 20-139 #domain signal sequence #status predicted #label SIG
 #product Ig heavy chain V region 129 #status predicted
 #label VAR
 #domain immunoglobulin homology #label IMM
 SUMMARY 34-117
 #length 139 #molecular_weight 15643 #checksum 5928

Query Match 68.4%; Score 683; DB 2; Length 139;
 Best Local Similarity 68.3%; Pred. No. 8.92e-102;
 Matches 95; Conservative 25; Mismatches 15; Indels 4; Gaps 3;

Db 1 MGNCMIFLFLSTAGVLSQVLOOQPGAEVYKPCASVYKSLCKSGYFTDTLHMVNR 60
 1 MGNCMIFLFLSTAGVLSQVLOOQPGAEVYKPCASVYKSLCKSGYFTDTLHMVNR 60
 1 MGNCMIFLFLSTAGVLSQVLOOQPGAEVYKPCASVYKSLCKSGYFTDTLHMVNR 60

QY 61 GQGLEWIGVINYIDNTNMYNKKFKATMTVDKSTAYMELSLRSDTAIVYCAR--A 118
 61 GQGLEWIGVINYIDNTNMYNKKFKATMTVDKSTAYMELSLRSDTAIVYCAR--A 118

Db 121 GRPYDWGOGTTLTVSS 137
 121 GRPYDWGOGTTLTVSS 137
 119 AWYMDYWGOGTTLTVSS 135

RESULT 10
 ENTRY PN0444 #type fragment
 TITLE Ig heavy chain V region precursor - human (fragment)
 ORGANISM Homo sapiens #common_name man
 DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999

ACCESSIONS PN0444
 REFERENCE PN0444
 #authors Kaluza, B.; Betzl, G.; Shao, H.; Diamantsehn, T.; Weidle,

U.H.
 Gene (1992) 122:321-328
 A general method for chimerization of monoclonal antibodies
 by inverse polymerase chain reaction which conserves
 authentic N-terminal sequences.

#journal
 #title
 #cross-references M01D:93138402
 #accession PN0444
 #molecule_type mRNA
 #residues 1-150 #label KAL
 #cross-references GB:102346
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 FEATURE 1-19
 20-150 #domain signal sequence #status predicted #label SIG
 #product Ig heavy chain V region #status predicted
 #label VAR
 #domain variable region #label VRG
 SUMMARY 20-117
 #length 150 #checksum 9720

Query Match 68.1%; Score 680; DB 2; Length 150;
 Best Local Similarity 66.4%; Pred. No. 3.25e-101;
 Matches 91; Conservative 26; Mismatches 18; Indels 2; Gaps 2;

Db 1 MEMSWIFLFLISGTAGVLSQVLOOQPGAEVYKPCASVYKSLCKSGYFTDTLHMVNR 60
 1 MEMSWIFLFLISGTAGVLSQVLOOQPGAEVYKPCASVYKSLCKSGYFTDTLHMVNR 60
 1 MGNCMIFLFLATATGVSQVLOOQPGAEVYKPCASVYKSLCKSGYFTDTLHMVNR 60

QY 61 GQGLEWIGVINYIDNTNMYNKKFKATMTVDKSTAYMELSLRSDTAIVYCAR--A 120
 61 GQGLEWIGVINYIDNTNMYNKKFKATMTVDKSTAYMELSLRSDTAIVYCAR--A 120

Db 121 GRPYDWGOGTTLTVSS 137
 121 GRPYDWGOGTTLTVSS 137
 121 -Y-MDYWGOGTTLTVSS 135

RESULT 11
 ENTRY MHMS18 #type complete
 TITLE Ig heavy chain precursor V region (B1-8) - mouse
 ORGANISM Mus musculus #common_name house mouse
 DATE 02-Apr-1992 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999

ACCESSIONS A90809; A22769; A02034; A02036
 REFERENCE A90809
 #authors Bothwell, A.L.M.; Pasikind, M.; Reith, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
 #journal Cell (1981) 24:625-637
 #title Heavy chain variable region contribution to the NP(b) family of antibodies: somatic mutation evident in a gamma2a variable region.
 #cross-references M01D:81234548
 #accession A90809
 #molecule_type DNA
 #residues 1-139 #label B18
 #cross-references GB:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115
 #accession B90809
 #molecule_type DNA
 #residues 1-117 #label 1862
 #note the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl (NPb antibodies) the 186-2 germline gene was cloned from a library of C57BL/6 DNA

REFERENCE A90971
 #authors Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
 #journal EMBO J. (1982) 1:635-640
 #title Immunoglobulin V region variants in hybridoma cells. II. Recombination between V genes.
 #cross-references M01D:84236026
 #accession A22769
 #molecule_type protein

20-139 ##label DIL
the V region of the B1-8 delta chain, derived as a
spontaneous class switch variant from the
IgM-producing B1-8 hybridoma, was partially sequenced
the sequence is identical with the V region of the mu
chain

```
#introns 16/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin
KEYWORDS heterotetramer; immunoglobulin
FEATURE
```

```

1-19      #domain signal sequence #status predicted #label SIG
20-139    #product i9 kappa chain v region (B1-8) #status
          experimental #label MAT\
34-117    #domain immunoglobulin homology #label IMM\
118-124   #region D segment\
125-139   #region J segment (JH2)
          #length i39 #molecular-weight 15419 #checksum 5229
SUMMARY

```

Best Local Similarity 88.3%; Pred. NO. 4.99e-101;
Matches 95; Conservative 24; Mismatches 16; Indels

[illegible]

ENTRY	#type fragment
TITLE	
Ig heavy chain precursor V region anti-idiotypic antibody	PL0208

ORGANISM DATE	ACCESIONS REFERENCE
E225 - mouse (strain BALB/c) (fragment) #mouse_name Mus musculus #common_name house mouse 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998	PL0208 PL0207
#journal #title	Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J. Mol. Immunol. (1990) 27:429-433 Nucleotide sequence of the VH, VL regions of an anti-idiotypic antibody reacting with a private idiotope of the anti-lysozyme D1.3 antibody.

```
##molecule_type mRNA
##residues 1-136 ##label SOU
```

```

#experimental_source hybridoma cell E255
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
FEATURE
1-19 #domain signal sequence #stratus predicted #label SIG
34-117 #domain immunoglobulin homology #label IMM\
50-54 #region complementarity-determining 1\
69-85 #region complementarity-determining 2\
118-125 #region complementarity-determining 3\
118-121 #region D region\
122-136 #region JH region
#length 136 #checksum 9740
SUMMARY

```

Best Local Similarity 66.9%; Pred. No. 7.6/e-101;
Matches 91; Conservative 26; Mismatches 18; Indels

Db 1 MGNNSFILEVATASGVYSQYQLQQPGSELVRRGASVKLSCKASGYTFITNYWMHWKQRP 60
||| :|||:|:| | | | | | :|:|: |||:|:| | | | | | :|||:|

QY 1 MGWNCIIFFELVTATGVHSQVLVOSGAEVKKPPGSSVKVSCKASGYTFTDYAIQWVRQAP 60

Db 61 GCGLEWIGNIYPGSGDSNYDEKEFSKATLTVDTSSTAYMQLSLGTSSEDSAVYYCARGLA 120

61 GCGLEWIGVINIYYDNTNYNQKFKGKATMTVDKSTSTAYMELSLRSED
 QY TAAYYCARA-A 119

Db 121 FYFDHWGQGTLLTVSS 136

ENTRY	RESULT	13
S31600	#type fragment	
Ig heavy chain V region -	human (fragment)	
#formal_name Homo sapiens	#common_name man	
22-Nov-1993	#sequence_revision 10	Nov-1995
23-Jul-1999	#text_change	

#authors
Cuisinier, A.M.; Gauchier, L.; Boubli, L.; Fougereau, M.;
Tonnelle, C.

#submission	submitted to the EMBL Data Library, June 1992
#description	Mechanisms that generate human immunoglobulin diversity
	operate from the 8th week of gestation in feral liver

```
##molecule_type mRNA
##residues      1-136 ##label CUT
#-----#format   rnr1_714155
```

```
#cross-tetrahetero EMBL:Z14103; NLD:G30994; PDB:1C6A/8534..1; PID:G30993
CLASSIFICATION #superfamily1 immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
34-117 #domain immunoglobulin homology #label IMM
SUMMARY #length 136 #checksum 9862
```

Best Local Similarity 71.3%; Pred. No. 1.81e-100;
Matches 97; Conservative 12; Mismatches 25; Indels

Dd 1 MDMMRILFLVLAATSAHSQVLVOSGAEYKKPGASYSKVSRCASGYMTSIDIMWVRQT 60
| | :
Oy 1 MGMNCLIFLVTTAIGHSQVLVOSGAEYKRPPSSYSKVSCKASGYFTFYDAIQWVRQP 60

01 Q Q U E M M O M I N F N S O N I G I A D N F Q G A V I M I K N I S I S I A I M E L S S K S E D I A V I I C A N R K D I Z U

01 GUGUENIGV INLI IDNININ

QY

DD 121 AF-DIMGUGIMV1V55 133
: | |||||: |||||

RESULT 14 .

ENTRY	F29380	#type	fragment	
TITLE	Ig heavy chain precursor V region (A003 40/567) - mouse (fragment)			
ORGANISM	#formal_name	Mus musculus	#common_name	house mouse
DATE	31-Dec-1988	#sequence_revision	31-Dec-1988	#text_changed
	23-Jul-1999			

```
#authors      Chen, H.T.; K
#journal      J. Biol. Chem
```

#title Nucleotide and translated amino acid sequences of cDNA coding for the variable regions of the light and heavy chains of mouse hybridoma antibodies to blood group A and B substances.

```
##molecule_type mRNA
##residues 1-137 ##label CHE
```

##cross-references GB:M1715; GB:J02815; NID:g195409; PIDN:AAA38294.1
PID:g195410

CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology		
KEYWORDS	heterotetramer; immunoglobulin		
FEATURE			
34-117			
SUMMARY	#domain immunoglobulin homology #label IMM		
Query Match	67.5%;	Score 674;	DB 2; Length 137;
Best Local Similarity	69.6%;	Pred. No.4,29e-100;	
Matches	96;	Conservative	20; Mismatches 18; Indels 4; Gaps 3;
Db	1	MGWMIILFLVATAGVSOVQOYQOQAEALVPGTISVKLSCKRAGNYFTYIMWVKLRP	60
Oy	1	MGWMIILFLVATAGVSOVQOYQOQAEALVPGTISVKLSCKRAGNYFTYIMWVKLRP	60
Db	61	GQGLEWIGDIDYPSGSGTNYNEKKSKATLTVDTSSTAYMOLSLASEDSALYTCARQV	120
Oy	61	GQGLEWIGVINIYDNTNYNQKFKGKATMTVDKSTSTAYMELSLRSEDTAYVYCAR--A	118
Db	121	ETWF-AYWGQTLVTYSA	137
Oy	119	-AWMTDYWGQTLVTYSS	135
RESULT	15		
ENTRY	T01407	#type fragment	
TITLE	Ig heavy chain (myeloma M104E) - mouse (fragment)		
ORGANISM	#formal_name Mus sp. #common_name mouse		
DATE	20-Sep-1999	#sequence_revision 20-Sep-1999 #text_change 20-Sep-1999	
ACCESSIONS	T01407		
REFERENCE	214317		
#authors	Takahashi, S.; Matsura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamamoto, Y.; Yamamoto, H.; Fujimoto, S.		
#journal	Microbiol. Immunol. (1992) 35:855-863		
#title	Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and anti-idiotypic antibodies involved in B-B cellular interaction.		
#cross-references	MUID:93116538		
#accession	T01407		
#status	translated from GB/EMBL/DBJ		
##molecule_type	mRNA		
##residues	1-140	#label TAK	
#cross-references	EMBL:S1851; NID:9262657; PID:e69004		
GENETICS			
#gene	M104E myeloma immunoglobulin heavy chain		
SUMMARY	#length 140 #checksum 7020		
Query Match	67.1%;	Score 670;	DB 2; Length 140;
Best Local Similarity	66.9%;	Pred. No.2,40e-99;	
Matches	91;	Conservative	22; Mismatches 22; Indels 1; Gaps 1;
Db	1	MGWMIILFLVATAGVSOVQOQOQAEALVPGTISVKLSCKRAGNYFTYIMWVKLRP	60
Oy	1	MGWMIILFLVATAGVSOVQOQOQAEALVPGTISVKLSCKRAGNYFTYIMWVKLRP	60
Db	61	GKSLWIGDIDPNNGGTSYNOKKRGKATLTVDKSSSTAYMOLSLASEDSALYTCARQV	120
Oy	61	GQGLEWIGVINIYDNTNYNQKFKGKATMTVDKSTSTAYMELSLRSEDTAYVYCAR-A	119
Db	121	WYPDWAGCTVTYSS	136
Oy	120	WYMDWGGQTLVTYSS	135

Search completed: Mon Aug 7 18:59:45 2000
Job time : 14 secs.


```

Oy      61 GCGLEMGIGVINYNTNNTNCKFKGKATVTDKSTSTAMMELSSRSEDTAVYYCAR-A 119
Db      121 NFFDYMGOGTTLTVSS 136
Oy      120 WYMDYMGOGTTLTVSS 135

RESULT 2
ID      HV01_MOUSE          STANDARD:          PRT:          137 AA.
DC      P01755.
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RP      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE: 81234548.
RA      Bothwell A.L.M., Paakind M., Reth M., Imansht-Karl T., Rajewsky K.,
RA      Baltimore D.;
RT      "Heavy chain variable region contribution to the NPB family of
RT      antibodies: somatic mutation evident in a gamma 2a variable region.";
RL      Cell 24:625-637(1981).
CC      -1- MISCELLANEOUS: THE GAMMA-2A CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC      MAKING ANTIBODIES TO THE HAPPEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC      (NPB ANTIBODIES).
CC      -----
CC      CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      CC      the European Bioinformatics Institute. There are no restrictions on its
CC      CC      use by non-profit institutions as long as its content is in no way
CC      CC      modified and this statement is not removed. Usage by and for commercial
CC      CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      CC      or send an email to license@isb-sib.ch).
CC      -----
DR      CCR      EMBL: J00539; AAA38172.1; -.
DR      DR      PIR: A02038; G2MS43.
DR      DR      PIRAN: PF00047; 1g; 1.
DR      DR      KW      Immunoglobulin V region; signal.
FT      FT      SIGNAL          1          19
FT      FT      CHAIN          20         137      IG HEAVY CHAIN V REGION S43.
FT      FT      DOMAIN         20         49      FRAMEWORK 1.
FT      FT      DOMAIN         50         54      COMPLEMENTARITY-DETERMINING 1.
FT      FT      DOMAIN         55         68      FRAMEWORK 2.
FT      FT      DOMAIN         69         85      COMPLEMENTARITY-DETERMINING 2.
FT      FT      DOMAIN         86         117      FRAMEWORK 3.
FT      FT      DOMAIN         118        122      D SEGMENT.
FT      FT      DOMAIN         123        137      JH2 SEGMENT.
FT      FT      DISULFID         41         115      BY SIMILARITY.
FT      FT      NON_TER         137        137
SO      SEQUENCE          137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match.          68.4%; Score 683; DB 1; Length 137;
Best Local Similarity 67.2%; Pred. No. 1,15e-135;
Matches 92; Conservative 23; Mismatches 20; Indels 2; Gaps 1;

Db      1 MGSMSIMFLIATATGCVHSVQVLOQPAEFYVPGASVKLSKASGYTFTSYLMMHWNP 60
Oy      1 MGNMNIIFFLVYTAAGVHSQVQVLYVSGAEVKKFGSGSVKASCASGITTFIDIAIQWRQAP 60
Db      61 GRGLEWIGRIDPNSGGTGYTNEHFRSKATLTIDKPSSTAYVMQLSLSLSEDSAVYYCARYL 120
Oy      61 GGGLEMGIGVINYNTNNTNCKFKGKATVTDKSTSTAMMELSSRSEDTAVYYCAR--A 118
Db      121 GRYFDYMGOGTTLTVSS 137
Oy      119 WYMDYMGOGTTLTVSS 135

RESULT 3
ID      HV07_MOUSE          STANDARD:          PRT:          139 AA.

```

```

AC P01751: P01752:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE: 81234548.
RA Bozhmova A.L.M., Peskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J00529; AAA38170.1; -.
DR PIR: A02034; MHMS16.
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
FT SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;
SQ
Query Match 68.0%; Score 679; DB 1; Length 139;
Best Local Similarity 68.3%; Pred. No. 1,128-134;
Matches 95; Conservative 24; Mismatches 16; Indels 4; Gaps 1;
Db 1 MGSWIMFLAATATAGVSHSOVLOQPGAEIVKPGASVYKSLCKASGYFTSYMMHMKVQRP 60
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 1 GGMWNIIFELVLTATAGVSHSOVLOVSGAEIVKPPSSVYKSVCKASGYFTPTDAIDWVRQAP 60
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 GRLGLEMIRIDPNSGGRYNNKFKSKATLYTDKRSSTAYIMOLSLTSDSAVYICARDY 120
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 GQGLEMIVIVYIDNNYNNKFKGKATMYDKSTFAYMELSSLRSDTAIVYICAR--- 117
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 121 YGSSYFDYWGQGTLLTVSS 139
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 118 -AAWIMDYWGQGTLLTVSS 135
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
RESULT 4
ID HVA8_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

```

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 84248078.
 RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
 RA Tucker P.W.:
 RT "Illegitimate recombination generates a class switch from C mu to C
 delta in an ID-secreting plasmacytoma."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
 DR PIR: A02033; HVM57.
 DR PIR: PF00047; Ig.1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
 FT DOMAIN 21 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 128 138 FRAMEWORK 4.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 138 138
 SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;
 Query Match 66.7%; Score 666; DB 1; Length 138;
 Best Local Similarity 68.1%; Pred. No. 1,84e-131;
 Matches 94; Conservative 20; Mismatches 21; Indels 3; Gaps 2;
 Db 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 QY 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 Db 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 120
 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 120
 QY 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 120
 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 120
 Db 121 YDWEYVWOGTLVPEFA 138
 1 YDWEYVWOGTLVPEFA 138
 QY 120 WY--MDYWGCGTLVTVSS 135
 120 WY--MDYWGCGTLVTVSS 135
 RESULT 5
 ID HV06_MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 102 PRECURSOR.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE: 81234548.
 RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.:
 RT "Heavy chain variable region contribution to the NPb family of
 antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 CC -I- MISCELLANEOUS; THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 DR PIR: A02033; HVM52.
 DR PIR: PF00047; Ig.1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
 Query Match 66.0%; Score 659; DB 1; Length 117;
 Best Local Similarity 76.7%; Pred. No. 9.87e-130;
 Matches 89; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 Db 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 QY 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 Db 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 116
 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 116
 QY 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 116
 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 116
 Db 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 117
 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 117
 QY 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 117
 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 117
 Query Match 64.7%; Score 646; DB 1; Length 117;
 Best Local Similarity 75.2%; Pred. No. 1.59e-126;
 Matches 88; Conservative 16; Mismatches 13; Indels 0; Gaps 0;
 Db 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 QY 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 1 MGNWCIIFLVATATDVHSHVSOVLQOPGAEIVKPGASVQSCSKASGTFPTNYIMHWKORP 60
 Db 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 117
 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 117
 QY 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 117
 61 GGGLEWIGINIVYDNTNOKFKKATLVKSSSTAYAMQSLSTSEDSAVYYCAR 117

Cell 24:625-637(1981).

- MISCELLANEOUS : THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

PIR: A02030; HMS23.1;
PFAM: PF00047; Ig; I.
Immunoglobulin v region: signal.

FT SIGNAL 1
KW CHAIN 19
FT CHAIN 20 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 FRAMEWORK 1.
FT DOMAIN 50 COMPLEMENTARITY - DETERMINING 1.
FT DOMAIN 55 FRAMEWORK 2.
FT DOMAIN 69 COMPLEMENTARITY - DETERMINING 2.
FT DOMAIN 86 FRAMEWORK 3.
FT DISULFID 41 BY SIMILARITY.
FT NON_TER 117

SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match Best Local Similarity 63.1%; Score 630; DB 1; Length 117;
Matches 84; Conservative 71.8%; Pred. No. 1,39e-122;
Mismatches 15; Indels 0; Gaps 0;

D_b 1 MGSWCIIFLVAANGVSHSVOLGPOPTGLVPASVKLSCKASGYTFSYMHWKORP 60
 |::||::||::||::||::||::||::||::||::||::||:
Oy 1 MGMNCIIFFLVTTATGVASHQVOLVGSAEYKKPPSSVSCKASGYTFDYAIQWRAP 60
 |||||||::||::||::||::||::||::||::||::||::||:

Dy 61 GGGEIWNIGNPGMGCGINYNKEFKSKVTYLIVDKSSSTAYTLOSLTSDESAVVICR 117
 |||||||::||::||::||::||::||::||::||::||::||:
Oy 61 GGCEIMGIWINYYDDNTNYNKRFKGAKMTVDKSTFYAMELSSLRSSEDIAYVICAR 117
 |||||||::||::||::||::||::||::||::||::||::||:

RESULT 9 STANDARD; PRT; 117 AA.

ID ID HVYG_HUMAN STANDARD; PRT; 117 AA.
AC AC P23083;
DT DT 01-NOV-1991 (Rel. 20, Created)
DT DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT DT 15-JUL-1991 (Rel. 38, Last annotation update)
DE DE IG HEAVY CHAIN V-I REGION V35 PRECURSOR.
OS OS Homo sapiens (Human).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN RN [1]
RP RP MEDLINE; 88296408.A.
RX RX Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA RA Ohno H., Fukushima S., Honjo T.;
RT RT "Dispersed localization of D segments in the human immunoglobulin heavy-chain locus."
RL RL EMBO J. 7:1047-1051(1988).C_c CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on ways CC CC use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb.sib.ch).
CC CC -----
DR DR EMBL; X07448; -. NOT ANNOTATED_CDS.
DR DR PIR: S00476; HIVHJ35.1;
DR DR PFAM: PF00047; Ig; I.
KW KW Immunoglobulin v region: Signal.
KM KM Immunoglobulin v region: Signal.
FT FT SIGNAL 1
FT CHAIN 19
FT NON_TER 20 IG HEAVY CHAIN V-I REGION V35.
FT NON_TER 117
SO SO SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match Best Local Similarity 62.7%; Score 626; DB 1; Length 117;
Matches 86; Conservative 73.5%; Pred. No. 1.35e-121;
Mismatches 9; Indels 0; Gaps 0;

D_b 1 MDWMRIIEFLVAAGTVGASVOVLVSGAEYKKPKPASVYSCKASGYTFGTGMHWKPAP 60
 |::||::||::||::||::||::||::||::||::||:
Oy 1 MGMCNIIFLLVITTAAGVSHSQVOLVGSAEYKKPGSSVSVCCKASGYTFDYAIQWRAP 60
 |||||||::||::||::||::||::||::||::||::||::||:


```

Db 61 GGGLEMMGRINPNSGGTNYAKFGARVTRDRTSISRAYMELSLRSDPTAVYYCAR 117
    |||||:| 11 ||| 111:| 11 ||||| 111:| 11111
QY 61 GGGLEMMIGVINITYNTNTNOKFKGKATMTVDKSTRAYMELSLRSDPTAVYYCAR 117

RESULT 10
ID HV49_MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JUN-1988 (Rel. 06, Created)
DT 01-JUN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85099340.
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
    unrearranged VH gene segments."
    Cell 40:271-281(1985).
RL -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
    or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: M13788; AAA38506.1; -
DR PIR: A02035; MHMSB4.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 58 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match
Best Local Similarity 62.5%; Score 624; DB 1; Length 117;
Matches 81; Conservative 22; Mismatches 14; Indels 0; Gaps 0;

Db 1 MGSCMCLFLAATATGVSPOVLOQPGAEVLKPGASVKLSCKSGYFTSYMHVWVQRP 60
    |||||:| 11 ||| 111:| 11 ||||| 111:| 11111
QY 1 MGNCNIIFFLVATATGVSQVLOVSGAEVKKPGSSVKSCASGYFTFYAIDQWVQRP 60
    |||||:| 11 ||| 111:| 11 ||||| 111:| 11111
DB 61 GGGLEMMIGTDPNPGSGKRYNKKFKATLVYDKPSSTAYMOLSLTSEDSAVYYCTR 117
    |||||:| 11 ||| 111:| 11 ||||| 111:| 11111
QY 61 GGGLEMMIGVINITYNTNTNOKFKGKATMTVDKSTRAYMELSLRSDPTAVYYCAR 117

RESULT 11
ID HV18_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83144028.

```

```

RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
    (VH) gene subgroups."
    Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
RL -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
    or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: J00240; AAA52988.1; -
DR PIR: A02024; HYH0HG.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match
Best Local Similarity 72.6%; Score 623; DB 1; Length 117;
Matches 85; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Db 1 MDNTWRFCLAVAPRAHSQVLOVSGAEVKKPGASVKSCASGYFTSYMHVWVQRP 60
    |||||:| 11 ||| 111:| 11 ||||| 111:| 11111
QY 1 MGNCNIIFFLVATATGVSQVLOVSGAEVKKPGSSVKSCASGYFTFYAIDQWVQRP 60
    |||||:| 11 ||| 111:| 11 ||||| 111:| 11111
DB 61 GGGLEMMIGTDPNPGSGKRYNKKFKATLVYDKPSSTAYMOLSLTSEDSAVYYCTR 117
    |||||:| 11 ||| 111:| 11 ||||| 111:| 11111
QY 61 GGGLEMMIGVINITYNTNTNOKFKGKATMTVDKSTRAYMELSLRSDPTAVYYCAR 117

RESULT 12
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1988 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN: C57BL/6;
RX MEDLINE: 81234548.
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NBP family of
    antibodies: somatic mutation evident in a gamma 2a variable region."
    Cell 24:625-637(1981).
RL -----
CC -1- RELATED GENES THAT COULD ENCODE V REGIONS OF NBP ANTIBODIES.
CC -----
DR PIR: B02034; HYMS61.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 58 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match
Best Local Similarity 70.1%; Score 622; DB 1; Length 117;
Matches 82; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

```

```

Db 1 MGNMCIIFLAAATGATGVSQVLOOQPGAEIVKPGASVYKLSKASGYFTFTYMMHWKORP 60
OY 1 MGNMCIIFLAAATGATGVSQVLOOQPGAEIVKPGASVYKLSKASGYFTFTYMMHWKORP 60
Db 61 GGGLEWIGRIDPNSGCTYNEKFKSKATLVDTSSSTAYMOLHSITSEDSAVYYCAR 117
OY 61 GGGLEWIGVINIYDNTNINYNOKFKGKATMTYDKSTAYMELSLRSBDAVYYCAR 117

RESULT 13
ID HVI4_MOUSE STANDARD; PRT: 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 108A PRECOURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81245215.
RA Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes."
RL Nature 292:426-430(1981).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC
CC EMBL; J00488; AAA38519.1; -.
DR PIR; A02041; HVM58A.
DR PFAM; PF00047; 1g; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 61.6%; Score 615; DB 1; Length 117;
Best Local Similarity 68.4%; Pred. No. 6, 83e-119;
Matches 80; Conservative 22; Mismatches 15; Indels 0; Gaps 0;

Db 1 MGNMCIIFLAAATGATGVSQVLOOQPGAEIVKPGASVYKLSKASGYFTFTYMMHWKORP 60
OY 1 MGNMCIIFLAAATGATGVSQVLOOQPGAEIVKPGASVYKLSKASGYFTFTYMMHWKORP 60
Db 61 GGGLEWIGRIDPNSGCTYNEKFKSKATLVDTSSSTAYMOLHSITSEDSAVYYCAR 117
OY 61 GGGLEWIGVINIYDNTNINYNOKFKGKATMTYDKSTAYMELSLRSBDAVYYCAR 117

RESULT 14
ID HVI4_MOUSE STANDARD; PRT: 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 145 PRECOURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6;
RX MEDLINE; 81234548.
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;

```

```

RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC
CC EMBL; J00533; AAA38602.1; -.
DR PIR; C02034; HVM45I.
DR PFAM; PF00047; 1g; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DEBA3F543E996 CRC64;

Query Match 61.1%; Score 610; DB 1; Length 117;
Best Local Similarity 69.2%; Pred. No. 1, 16e-117;
Matches 81; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

Db 1 MGNMCIIFLAAATGATGVSQVLOOQPGAEIVKPGASVYKLSKASGYFTFTYMMHWKORP 60
OY 1 MGNMCIIFLAAATGATGVSQVLOOQPGAEIVKPGASVYKLSKASGYFTFTYMMHWKORP 60
Db 61 GGGLEWIGRIDPNSGCTYNEKFKSKATLVDTSSSTAYMOLHSITSEDSAVYYCAR 117
OY 61 GGGLEWIGVINIYDNTNINYNOKFKGKATMTYDKSTAYMELSLRSBDAVYYCAR 117

RESULT 15
ID HVI2_MOUSE STANDARD; PRT: 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 83075344.
RA Kehry M.R., Fuhman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains."
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; HVM54E.
DR PFAM; PF00047; 1g; 1.
DR Immunoglobulin V region; Glycoprotein.
RW DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACF4BEA47E41 CRC64;

Query Match 59.6%; Score 595; DB 1; Length 117;
Best Local Similarity 70.1%; Pred. No. 5, 54e-114;
Matches 82; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

```

Sun Aug 27 09:11:04 2000

US-09-249-011-6.rsp

Page 7

Db 1 EYVLOOQSEPELVYKSPASVKMSKAGSAGTFTDYKMMKQVSHKSLSEWIGDIPNNNGSY 60
 QY 20 QVQLVQSAEYKPKPSSYKVKSCKAGSYFTDIAIQWVKNQAPQGLEMLIVINITYIDNTY 79
 Db 61 NQKFKGKTLTVYDKSSSTAYKQNLNLTSPDSAVYYCARDIYKFDYWGAGITVYSS 117
 QY 80 NQKFKGKTLTVYDKSTALNELSLRSIEDIYVCAH-AITMDIYWGGLITVYSS 135

```
Search completed: Mon Aug 7 18:58:33 2000
Job time : 9 secs.
```

 W P S R E H
 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

MParch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Aug 7 19:00:01 2000; MasPar time 10.25 Seconds
 Tabular output not generated. 312.013 Million cell updates/sec

Title: >US-09-249-011-6
 Description: (1-135) from US09249011.pep
 Perfect Score: 999
 Sequence: 1 MGNMCIFFLVLTATGVHSQ.....ARAAHYNDYNGCGLVTVSS 135

Scoring table:
 PAM 150
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq36
 1:geneseqp

Statistics: Mean 30.791; Variance 156.235; scale 0.197

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description	Pred. No.
1	786	78.7	588	1 W71880 Anti-human Fas humanis	9.69e-54
2	772	77.3	140	1 R55556 DRG-200 Humanized ant	1.40e-52
3	770	77.1	470	1 W83037 Anti-Fas humanized ant	2.04e-52
4	759	76.0	588	1 W71881 Anti-human Fas humanis	1.66e-51
5	755	75.6	145	1 W83038 Anti-Fas humanized ant	3.56e-51
6	755	75.6	470	1 W83036 Anti-Fas humanized ant	3.56e-51
7	753	75.4	135	1 R24107 Humanised anti-Fac ant	5.21e-51
8	753	75.4	136	1 R59512 Sequence of the heavy	5.21e-51
9	750	75.1	163	1 R15060 Murine anti-ICAM monoc	9.22e-51
10	750	75.1	163	1 R15200 R6-5-D6 anti-ICAM-1 he	9.22e-51
11	748	74.9	135	1 R06369 Anti-Fac heavy chain v	1.35e-50
12	747	74.8	135	1 R29017 pUC-RVh-1220d.	1.63e-50
13	745	74.6	135	1 R29016 pUC-RVh-1220d.	2.39e-50
14	745	74.6	136	1 W06442 Hmuc3 VH region.	2.39e-50
15	737	73.8	133	1 R81840 E-selectin CDR-grafted	1.09e-49
16	737	73.8	134	1 R06250 Variable region of mur	1.09e-49
17	737	73.8	140	1 W21847 Humanised heavy chain	1.09e-49
18	721	72.2	139	1 W36165 Humanised heavy chain	2.30e-48
19	719	72.0	140	1 W21849 Humanised heavy chain	3.36e-48
20	718	71.9	180	1 W53813 Heavy chain of a human	4.06e-48
21	717	71.8	140	1 W21850 Humanised heavy chain	4.91e-48
22	709	71.0	136	1 W10239 Chimeric anti-hepatiti	2.25e-47
23	709	71.0	136	1 W89535 Chimeric anti-hepatiti	2.25e-47

24	709	71.0	136	1	W16340	Mouse-human chimeric	2.25e-47
25	709	71.0	136 <td>1</td> <td>W10584</td> <td>Anti-hepatitis B heavy</td> <td>2.25e-47</td>	1	W10584	Anti-hepatitis B heavy	2.25e-47
26	709	71.0	136 <td>1</td> <td>W47517</td> <td>Human anti-hepatitis a</td> <td>2.25e-47</td>	1	W47517	Human anti-hepatitis a	2.25e-47
27	709	71.0	136 <td>1</td> <td>W47510</td> <td>Human anti-hepatitis a</td> <td>2.25e-47</td>	1	W47510	Human anti-hepatitis a	2.25e-47
28	709	71.0	136 <td>1</td> <td>P70624</td> <td>Sequence encoded by an</td> <td>2.25e-47</td>	1	P70624	Sequence encoded by an	2.25e-47
29	709	71.0	136 <td>1</td> <td>W41054</td> <td>Human anti-hepatitis a</td> <td>2.25e-47</td>	1	W41054	Human anti-hepatitis a	2.25e-47
30	709	71.0	144 <td>1</td> <td>W73187</td> <td>Fragment of gangliosid</td> <td>2.25e-47</td>	1	W73187	Fragment of gangliosid	2.25e-47
31	707	70.8	139 <td>1</td> <td>W29753</td> <td>CDR-grafted humanised</td> <td>3.28e-47</td>	1	W29753	CDR-grafted humanised	3.28e-47
32	707	70.8	139 <td>1</td> <td>R33953</td> <td>gH1 variable domain.</td> <td>3.28e-47</td>	1	R33953	gH1 variable domain.	3.28e-47
33	707	70.8	140 <td>1</td> <td>W21851</td> <td>Humanised heavy chain</td> <td>3.28e-47</td>	1	W21851	Humanised heavy chain	3.28e-47
34	705	70.6	140 <td>1</td> <td>W53815</td> <td>Murine Act-1 heavy cha</td> <td>4.80e-47</td>	1	W53815	Murine Act-1 heavy cha	4.80e-47
35	703	70.4	139 <td>1</td> <td>W62205</td> <td>Humanised anti-HM1.24</td> <td>7.02e-47</td>	1	W62205	Humanised anti-HM1.24	7.02e-47
36	703	70.4	139 <td>1</td> <td>W65773</td> <td>Anti-human HM1.24 anti</td> <td>7.02e-47</td>	1	W65773	Anti-human HM1.24 anti	7.02e-47
37	703	70.4	140 <td>1</td> <td>W77294</td> <td>HM1.24 antibody heavy</td> <td>7.02e-47</td>	1	W77294	HM1.24 antibody heavy	7.02e-47
38	703	70.4	144 <td>1</td> <td>W73172</td> <td>Heavy chain of ganglio</td> <td>7.02e-47</td>	1	W73172	Heavy chain of ganglio	7.02e-47
39	702	70.3	139 <td>1</td> <td>W62212</td> <td>Humanised anti-HM1.24</td> <td>8.49e-47</td>	1	W62212	Humanised anti-HM1.24	8.49e-47
40	702	70.3	144 <td>1</td> <td>W73189</td> <td>Fragment of gangliosid</td> <td>8.49e-47</td>	1	W73189	Fragment of gangliosid	8.49e-47
41	699	70.0	136 <td>1</td> <td>W1818</td> <td>Humanised mouse anti-h</td> <td>1.50e-46</td>	1	W1818	Humanised mouse anti-h	1.50e-46
42	699	70.0	136 <td>1</td> <td>W60036</td> <td>Human antibody F919 he</td> <td>1.50e-46</td>	1	W60036	Human antibody F919 he	1.50e-46
43	699	70.0	139 <td>1</td> <td>W62211</td> <td>Humanised anti-HM1.24</td> <td>1.50e-46</td>	1	W62211	Humanised anti-HM1.24	1.50e-46
44	697	69.8	135 <td>1</td> <td>W60866</td> <td>Variable region of an</td> <td>2.19e-46</td>	1	W60866	Variable region of an	2.19e-46
45	697	69.8	590 <td>1</td> <td>W31751</td> <td>H chain subunit of Fas</td> <td>2.19e-46</td>	1	W31751	H chain subunit of Fas	2.19e-46

ALIGNMENTS

RESULT	1	ALIGNMENTS
ID	W71880 standard; Protein; 588 AA.	
AC	W71880;	
DT	18-JAN-1999 (first entry)	
DE	Anti-human Fas humanised antibody CH11 heavy chain HmH.	
KM	Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;	
KW	autoimmune disease; rheumatoid arthritis; therapy; human;	
OS	Human antibody engineering.	
OS	Homo sapiens.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	Peptide	1..19
FT	Protein	/label= Sig-peptide
FT		20..588
FT		/label= Mat-protein
FT	Region	50..54
FT		/label= CDR1
FT		/note= "Complementarity determining region 1 from CH11 heavy chain"
FT	Region	69..84
FT		/label= CDR2
FT		/note= "Complementarity determining region 2 from CH11 heavy chain"
FT	Region	118..124
FT		/label= CDR3
FT		/note= "Complementarity determining region 3 from CH11 heavy chain"
EP	866131-A2.	
PD	23-SEP-1998.	
PD	20-MAR-1998.	
PD	21-MAR-1997.	
PA	(SANY) SANKYO CO LTD.	
PI	Haruyama H, Nakahara K, Serizawa N, Takahashi T,	
PI	Yonehara S;	
DR	WPI: 98-482965/42.	
DR	N-PSDB; V61363.	
PT	Production of anti-Fas protein humanised antibodies - for use in	
PT	inducing apoptosis on Fas expressing cells in the treatment of	
PT	autoimmune diseases, especially rheumatoid arthritis	
PS	Claim 21; Page 105-107; 187pp; English.	
CC	This is the amino acid sequence of a humanised anti-Fas antibody	
CC	CH11 heavy chain, designated HmH. HmH is based on the heavy	
CC	chain (see W71888) of murine anti-human Fas monoclonal antibody	
CC	CH11. The humanised sequence was designed following selection of	
CC	donor residues from CH11 to be grafted onto acceptor molecule	
CC	21.28/CL. 2 Heavy chain sequences (see W71880-81) have been	
CC	designed, and each can be used in combination with any of 4	

CC light chain sequences (see W71876-79) to provide novel, claimed
 CC humanised CH1 IGM antibodies that lack a J chain. These humanised
 CC anti-human Fas antibodies are capable of inducing apoptosis in cells
 CC expressing Fas (e.g. synovocytes) and are useful in the treatment
 CC of autoimmune disease and chronic rheumatoid arthritis. DNA
 CC sequences encoding the humanised antibodies are claimed, as are
 CC vectors such as pMNH5-1 including the HmuH nucleotide sequence
 CC (see V61363), and host cells such as Escherichia coli pMNH5-1
 CC (FERM BP-5863).
 CC Sequence 388 AA:

Query Match 78.7%; Score 786; DB 1; Length 588;

Best Local Similarity 77.8%; Pred. No. 9,69e-54;
 Matches 105; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

DB 1 MGSMTFLFLSGTAGVHSEVOLVOSGAEVKPKGASVSKASGTYTDDYMHVRAAP 60
 QY 1 MGSMTFLFLSGTAGVHSEVOLVOSGAEVKPKGASVSKASGTYTDDYMHVRAAP 60
 DB 61 GGGLEWIGYINITYDNTNOKFKATLTVDNSATFAMELSLRSDTAVYCARAAW 120
 QY 61 GGGLEWIGYINITYDNTNOKFKATLTVDNSATFAMELSLRSDTAVYCARAAW 120
 DB 121 AMDYWGQGLTVTVSS 135
 QY 121 YMDYWGQGLTVTVSS 135

RESULT 2
 ID R55556 standard; Protein: 140 AA.
 AC R55556;

DE 16-NOV-1994 (first entry)
 DE DREG-200 Humanized antibody heavy chain variable region.
 KW DREG-200; L-selectin; LECAM-1; Mel-14; LAM-1;
 KW humanized antibody; immunoglobulin; Ig; IgG1; IgG4;
 KW complementarity determining region; CDR; monoclonal antibody; MAb;
 KW framework; light chain; heavy chain; variable domain;
 KW monoclonal antibody; acceptor antibody Bu; transgenic animal.
 OS Mus sp.; Homo sapiens.

FT Key Location/Qualifiers
 FT peptide 1..19
 FT /label= Sig_peptide
 FT region 50..54
 FT /label= CDR1
 FT region 69..85
 FT /label= CDR2
 FT region 118..129
 FT /label= CDR3
 FT region
 FT WO9412215-A.
 PN 09-JUN-1994.
 PD 30-NOV-1993. U11612.
 PF 01-DEC-1992; US-983946.
 PR (PROT-) PROTEIN DESIGN LABS INC.
 PA Co MS;
 PI WPI: 94-199974/24.
 DR P-PSDB: 066702.
 PT New humanised antibody specific for L-selectin - with murine CDR
 PT and human framework regions, inhibits binding of neutrophils to
 PT endothelial cells and useful for treating or preventing
 PT inflammation
 PT Disclamaure; Fig. 3B; 60pp; English.
 PS An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs
 CC corresponding to those of mouse MAb DREG-200 and heavy and light
 CC chain variable region frameworks of the human acceptor antibody Bu.
 CC Nucleotide and aa sequences are provided for the DREG-200 light
 CC (Q66699), R55553 and heavy (Q66700, R55554) chain variable regions
 CC and the humanized DREG-200 light (Q66701, R55555) and heavy (Q66702,
 CC R55556) chain variable regions. The humanized antibodies can be
 CC produced economically in large quantities by expression in mammalian
 CC cell culture or in transgenic animals.
 CC Sequence 140 AA:

Query Match 77.3%; Score 772; DB 1; Length 140;

Best Local Similarity 78.6%; Pred. No. 1.40e-52;
 Matches 110; Conservative 11; Mismatches 14; Indels 5; Gaps 2;

DB 1 MGSMTFLFLSGTAGVHSEVOLVOSGAEVKPKGASVSKASGTYTDDYMHVRAAP 60
 QY 1 MGSMTFLFLSGTAGVHSEVOLVOSGAEVKPKGASVSKASGTYTDDYMHVRAAP 60
 DB 61 GGGLEWIGYINITYDNTNOKFKATLTVDNSATFAMELSLRSDTAVYCARAAW 120
 QY 61 GGGLEWIGYINITYDNTNOKFKATLTVDNSATFAMELSLRSDTAVYCARAAW 120
 DB 121 GNYVYFDPWQGLTVTVSS 140
 QY 121 --YMDY--WGQGLTVTVSS 135

RESULT 3
 ID W83037 standard; Protein: 470 AA.
 AC W83037;

DE 15-MAR-1999 (first entry)
 DE Anti-Fas humanised antibody HEF7A heavy chain.
 KW HEF7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HEF7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers
 FT peptide 1..19
 FT /label= Sig_peptide
 FT protein 20..470
 FT /label= Mat_protein
 FT region 20..140
 FT /label= Variable
 FT region 141..464
 FT /label= Constant
 FT region 50..54
 FT /label= CDR_H1
 FT /note= "claim 9"
 FT region 69..84
 FT /label= CDR_H2
 FT /note= "claim 9"
 FT region 118..129
 FT /label= CDR_H3
 FT /note= "claim 9"

PN AU9859701-A.
 PD 08-OCT-1998.
 PF 30-MAR-1998; 059701.
 PR 08-OCT-1997; JP-276064.
 PR 01-APR-1997; JP-082953.
 PR 25-JUN-1997; JP-169088.
 PA (SANTY) SANKYO CO LTD.
 PI Akio S, Hideyuki H./ Hiroko Y, Jun O, Kimihisa I,
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 DR WPI: 98-543440/47.
 DR N-PSDB: V70080.
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 PS Claim 22: Page 225-227; 292pp; English.
 CC This is the amino acid sequence of the HV type humanised heavy
 CC chain of murine anti-human Fas monoclonal antibody HEF7A. It
 CC includes humanising R44G and A76T amino acid substitutions that are
 CC conserved in the human IgG heavy chain. Host Escherichia coli
 CC pGHPDHV3 SANK 70298 harbors plasmid pGHPDHV3 carrying a fusion

PF 30-MAR-1998; 059701.
 PR 08-OCT-1997; JP-276064.
 PR 01-APR-1997; JP-082953.
 PR 25-JUN-1997; JP-169088.
 PA (SANKY) SANKYO CO LTD.
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I,
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 DR WPI: 98-543440/47.
 DR N-PSDB: V70104.
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 PS Example 3; Page 207; 292pp; English.
 CC This is the amino acid sequence of the VD type humanised heavy
 CC chain variable region of murine anti-human Fas monoclonal antibody
 CC HEF7A. It was utilised in a claimed humanised HEF7A heavy chain
 CC (see V70079). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HEF7A (see
 CC W83033-37) are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. Humanised antibodies are used to evaluate, in animal models,
 CC treatments of diseases that involve Fas/Fas ligand interactions, and
 CC also to treat such diseases, including autoimmune disease (e.g.
 CC systemic lupus erythematosus, Hashimoto's disease, graft versus host
 CC disease, Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 SQ Sequence 145 AA;

Query Match 75.6%; Score 755; DB 1; Length 145;
 Best Local Similarity 78.6%; Pred. No. 3,56e-51;
 Matches 110; Conservative 12; Mismatches 13; Indels 5; Gaps 2;

Db 1 MGMSCTILFLVATAGVHSQVQLVQSGAEVKKPGASVVSVCASGYTFTSYMQRVQAP 60
 QY 1 MGWNCIIFFLVTTAGVHSQVQLVQSGAEVKKPGSSVVSVCASGYTFTDAIQWVRQAP 60
 Db 61 GORLEMEIGIPSDSYTYNOKFKGKATLVDTSTASTAYMELSLRSEDYAVYYCARND 120
 QY 61 GOGLEWIGIVINYYDNTNINOKFKGKATLVDTSTASTAYMELSLRSEDYAVYYCARA-- 118
 Db 121 YSNMNYFDVWEGTGLVTVSS 140
 QY 119 -A-WYMDYWGCGTLVTVSS 135

RESULT 6
 ID W83036 standard; Protein: 470 AA.
 AC W83036;
 DT 15-MAR-1999 (first entry)
 DE Anti-Fas humanised antibody HEF7A heavy chain.
 KW HEF7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HEF7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 OS Homo sapiens.
 OS Synthetic.
 FH Key
 FT Peptide
 FT 1.19
 FT Location/Qualifiers
 FT /Label= Sig_peptide
 FT 20..470
 FT Protein

FT /Label= Mat_protein
 FT 20..140
 FT Region
 FT /Label= Variable
 FT 141..464
 FT Region
 FT /Label= Constant
 FT 50..54
 FT Region
 FT /Label= CDR_H1
 FT /note= "claim 9"
 FT 69..84
 FT Region
 FT /Label= CDR_H2
 FT /note= "claim 9"
 FT 118..129
 FT Region
 FT /Label= CDR_H3
 FT /note= "claim 9"
 FT
 PN AU9859701-A.
 PD 08-OCT-1998.
 PF 30-MAR-1998; 059701.
 PR 08-OCT-1997; JP-276064.
 PR 01-APR-1997; JP-082953.
 PR 25-JUN-1997; JP-169088.
 PA (SANKY) SANKYO CO LTD.
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I,
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 DR WPI: 98-543440/47.
 DR N-PSDB: V70079.
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 PS Claim 22; Page 212-213; 292pp; English.
 CC This is the amino acid sequence of the VD type humanised heavy
 CC chain of murine anti-human Fas monoclonal antibody HEF7A. E. coli
 CC pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion
 CC fragment of the humanised VD type HEF7A heavy chain and DNA
 CC encoding human IgG1 constant region (see V70079), and is deposited
 CC as FERM BP-6074 (claimed). The invention provides methods for
 CC producing humanised antibodies by culturing host cells. Humanised
 CC versions of HEF7A (see W83033-37), like native HEF7A, are capable
 CC of inducing apoptosis in abnormal cells expressing Fas, and of
 CC inhibiting Fas-induced apoptosis in normal cells. The humanised
 CC antibodies are used to evaluate, in animal models, treatments of
 CC diseases that involve Fas/Fas ligand interactions, and also to
 CC treat such diseases, including autoimmune disease (e.g. systemic
 CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
 CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
 CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
 CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 SQ Sequence 470 AA;

Query Match 75.6%; Score 755; DB 1; Length 470;
 Best Local Similarity 78.6%; Pred. No. 3,56e-51;
 Matches 110; Conservative 12; Mismatches 13; Indels 5; Gaps 2;

Db 1 MGMSCTILFLVATAGVHSQVQLVQSGAEVKKPGASVVSVCASGYTFTSYMQRVQAP 60
 QY 1 MGWNCIIFFLVTTAGVHSQVQLVQSGAEVKKPGSSVVSVCASGYTFTDAIQWVRQAP 60
 Db 61 GORLEMEIGIPSDSYTYNOKFKGKATLVDTSTASTAYMELSLRSEDYAVYYCARND 120
 QY 61 GOGLEWIGIVINYYDNTNINOKFKGKATLVDTSTASTAYMELSLRSEDYAVYYCARA-- 118
 Db 121 YSNMNYFDVWEGTGLVTVSS 140
 QY 119 -A-WYMDYWGCGTLVTVSS 135

RESULT 7
 ID R24107 standard; Protein: 135 AA.
 AC R24107;

DT 25-NOV-1992 (first entry)
 DE Humanised anti-Tac antibody heavy chain.
 KM Immunoglobulin; T cell related diseases; leukemia; autoimmune;
 OS IL-2 receptor; recombinant; diagnosis; therapy.
 FH Synthetic.
 FT Key
 FT Location/Qualifiers
 FT 1. 19
 FT /note- "signal peptide"
 FT 20. 135
 FT /note- "mature peptide"
 FT Peptide
 PD DD-296964-A.
 PD 19-DEC-1991.
 PF 17-JAN-1990; 337159.
 PR 17-JAN-1990; DD-337159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Queen CL, Selick HE;
 DR WPI; 92-167794/21.
 DR N-PSDB; Q24790.
 PT New humanised antibody specific for interleukin-2 receptor - with
 PT complementarity determ. regions and framework from different
 PT immunoglobulin(s), is non immunogenic and used to treat T-cell
 PT mediated disorders
 PS Disclosure; Fig 3; 21pp; German.
 CC The sequence is that of the humanised anti-Tac antibody heavy chain
 CC which is used in the production of a human-type immunoglobulin (19)
 CC that reacts specifically with p55-Tac protein and/or inhibits binding
 CC of human interleukin-2 (IL-2) to its specific receptor. The three
 CC complementarity determining regions and amino acids 27, 30, 48, 67,
 CC 68, 93, 95, 98, 107, 108, 109 and 111 of human antibody Eu have been
 CC replaced with the corresponding amino acids in the anti-Tac heavy chain
 CC antibody. This produces a humanised antibody which has the same
 CC affinity as anti-Tac for IL-2 receptors. The Ig may be used to treat
 CC humans with T-cell related diseases such as transplant rejection,
 CC T cell leukemia, or autoimmune diseases such as diabetes or multiple
 CC sclerosis. See also R24103-R24108.
 CC Sequence 135 AA:
 SQ
 Query Match 75.4%; Score 753; DB 1; Length 135;
 Best Local Similarity 77.8%; Pred. No. 5.21e-51;
 Matches 105; Conservative 15; Mismatches 15; Indels 0; Gaps 0;
 Db 1 MGNMWIFLFLSLGAGVHSGVOLVQSGAEVKKPGSSVYKSCAKSGYFTSTYIMHWKAP 60
 QY 1 MGNWCIFFPLVTTATGVHSGVOLVQSGAEVKKPGSSVYKSCAKSGYFTSTYIMHWKAP 60
 Db 61 GQGLEWIGVNIINPSTGYEYNQKFKDRTTADSTNTAYNELSLRSEDPAVYYCARGCG 120
 QY 61 GQGLEWIGVNIINPSTGYEYNQKFKDRTTADSTNTAYNELSLRSEDPAVYYCARGCG 120
 Db 121 VFDPYWGQGLTVTVSS 135
 QY 121 VFDPYWGQGLTVTVSS 135
 QY 121 YMDYWGQGLTVTVSS 135
 RESULT 8
 ID R59512 standard; Protein; 136 AA.
 AC R59512;
 DT 31-DEC-1994 (first entry)
 DE Sequence of the heavy chain variable region of the
 DE humanised NA-8 antibody including signal sequence.
 KM Humanised antibody; NA-8; human CD18; complementarity determining region;
 OS CDR.
 FH Synthetic.
 FT Location/Qualifiers
 FT 1. 19
 FT /label= leader
 FT 50. 54
 FT /label= CDR1
 FT 69. 85
 FT /label= CDR2
 FT 118. 127
 FT /label= CDR3
 FT 139. 163
 FT domain /label= constant
 PD WQ9116927-A.
 PD 14-NOV-1991.
 PF 29-APR-1991; U02942.
 PR 27-APR-1990; GB-009549.
 PA (CELL-) CELTECH LTD.
 PA (BOEH) BOEHRINGER INGELHEIM PHA.
 PI Abair JR, Ahtwal DS, Rothlein RA;
 DR WPI; 91-353533/48.
 DR N-PSDB; Q14802.
 PT New humanised CDR-grafted anti-ICAM antibodies - used to treat
 PT murine antibody NA-8, prevent binding of neutrophils to

PT endothelial cells, useful for treating inflammation
 PS Example; Fig 3b; 50pp; English.
 CC The mouse antibody NA-8 binds to human CD18. CDNA's for the heavy
 CC chain and light chain variable domain genes of NA-8 were cloned
 CC using anchored PCR. The cDNA variable domain sequences and the
 CC deduced AA sequences are shown in Q66845/R59509 and Q66846/R59510.
 CC The antibody Eu was chosen to provide the framework sequence for
 CC the humanisation of NA-8. At each posn. the AA was chosen to be the
 CC same as in the Eu antibody unless that posn. was 1) in a CDR, 11)
 CC the Eu AA was atypical whilst the NA-8 AA was typical for human
 CC antibodies in that posn.; 111) immediately adjacent to a CDR; 1v)
 CC the AA was physically close to the CDR. In addition the AA from NA-8
 CC was chosen at light chain posn. 49 because it was at the light-
 CC heavy chain interface. Humanised NA-8a has the same light chain
 CC as humanised NA-8 but in the heavy chain the human Eu AAs were
 CC retained as posns 67, 68, 70 and 74 rather than being replaced by
 CC the murine NA-8 AAs. Humanised NA-8a was used to determine whether
 CC these AAs were imp. in maintaining binding affinity. For the
 CC construction of genes for the humanised antibodies, nucleotide
 CC sequences were selected that encode the protein sequences of the
 CC humanised heavy and light chains, including signal peptides,
 CC generally using codons found in the mouse sequence. The gene
 CC sequence also include splice donor signals and an XbaI site at
 CC each end (See Q66847/R59511 and Q66848/R59512).
 CC Sequence 136 AA:
 SQ
 Query Match 75.4%; Score 753; DB 1; Length 136;
 Best Local Similarity 75.7%; Pred. No. 5.21e-51;
 Matches 103; Conservative 19; Mismatches 13; Indels 1; Gaps 1;
 Db 1 MGNMWIFLFLSLGAGVHSGVOLVQSGAEVKKPGSSVYKSCAKSGYFTSTYIMHWKAP 60
 QY 1 MGNWCIFFPLVTTATGVHSGVOLVQSGAEVKKPGSSVYKSCAKSGYFTSTYIMHWKAP 60
 Db 61 GQGLEWIGVNIINPSTGYEYNQKFKDRTTADSTNTAYNELSLRSEDPAVYYCARGCG 120
 QY 61 GQGLEWIGVNIINPSTGYEYNQKFKDRTTADSTNTAYNELSLRSEDPAVYYCARGCG 120
 Db 121 VFDPYWGQGLTVTVSS 136
 QY 121 VFDPYWGQGLTVTVSS 136
 QY 121 YMDYWGQGLTVTVSS 135
 RESULT 9
 ID R15060 standard; Protein; 163 AA.
 AC R15060;
 DT 13-FEB-1992 (first entry)
 DE Murine anti-ICAM monoclonal antibody heavy chain.
 KM Intercellular adhesion molecule; variable region; (VH); mouse;
 KM R5-5-D6 murine Mab; complementarity determining region; CDR.
 OS Mus musculus.
 FH Key
 FT Location/Qualifiers
 FT 1. 19
 FT /label= leader
 FT 50. 54
 FT /label= CDR1
 FT 69. 85
 FT /label= CDR2
 FT 118. 127
 FT /label= CDR3
 FT 139. 163
 FT domain /label= constant
 PD WQ9116927-A.
 PD 14-NOV-1991.
 PF 29-APR-1991; U02942.
 PR 27-APR-1990; GB-009549.
 PA (CELL-) CELTECH LTD.
 PA (BOEH) BOEHRINGER INGELHEIM PHA.
 PI Abair JR, Ahtwal DS, Rothlein RA;
 DR WPI; 91-353533/48.
 DR N-PSDB; Q14802.
 PT New humanised CDR-grafted anti-ICAM antibodies - used to treat
 PT and prevent inflammation (e.g. psoriasis) tumours, viral

PT Infections and asthma and in diagnosis
PS Disclosure: Fig 2: 83pp; English.
CC The heavy chain coding sequence was isolated from a cDNA library
CC prep'd. from hybridoma cell line R6-5-D6 which secretes murine
CC IgG2a/kappa antibody. The library was screened using a 960bp
CC BamHI-EcoRI fragment of a previously isolated mouse IgG2a constant
CC region clone. The murine framework-encoding sequences (i.e. not
CC encoding CDRs) will be replaced by human framework sequences to
CC produce recombinant (CDR-grafted humanised) antibody molecules
CC having specificity for ICAM-1.
SQ Sequence 163 AA;
Query Match 75.1%; Score 750; DB 1; Length 163;
Best Local Similarity 70.3%; Pred. No. 9,22e-51;
Matches 97; Conservative 25; Mismatches 13; Indels 3; Gaps 1;
Db 1 MGMSCTFFLVATATGHSQVQLQSGPELVKPGYVKRISKSGSYTFDAIHVKESH 60
QY 1 MGWNCIIFFLVTTATGHSQVQLVQSGAEVKKRPGSSVKVSKASGYTFDYAIQWVRAP 60
DB 61 AKSLKMGIVISAGDTNYNOKFKKATMTVDKSSNTAYLELRLTSEDSATYYCARGGW 120
QY 61 GGGLEWIGIVINITYDNTYNOKFKKATMTVDKSTSTAYMELSSLRSEDTAVYICARAAW 120
Db 121 LLSFDYWGQGTTLTVSS 138
QY 121 YM---DYWGQGTTLTVSS 135
RESULT 10
ID R15200 standard; Protein: 163 AA.
AC R15200;
DT 14-FEB-1992 (first entry)
DE R6-5-D6 anti-ICAM-1 heavy chain.
KW Interleukin adhesion molecule-1; antibody; chimaeric.
OS Mus musculus.
FH Key Location/Qualifiers
FT peptide 1..19
FT /label= signal_sequence
FT region 50..54
FT /label= CDR
FT region 69..85
FT /label= CDR
FT region 118..127
FT /label= CDR
FT region 139..149
FT /label= CDR
FT region 150..163
FT /label= constant_domain
FN MO9116928-A.
PN 14-NOV-1991.
PD 29-APR-1991; U02946.
PR 27-APR-1990; GB-009548.
PA (CELL-) CELTECH LTD.
PI (BOHR) BOEHRINGER INGELHEIM PHA.
PI Adair JR, Robinson MK, Bright SM, Rothlein RA;
DR WPI: 91-353534/48.
DR N-PSDB: 014652.
PT New humanised chimeric anti-ICAM-1 antibodies - useful in
PT treating inflammation e.g. psoriasis and ulcerative colitis to
PT suppress metastasis of haematopoietic tumour cell and in
PT diagnosis.
PS Disclosure: Fig 2: 85pp; English.
CC The sequence comprises the signal sequence, variable region and part
CC of the constant region for the R6-5-D6 murine MAB heavy chain. The
CC hybridoma cell line R6-5-D6 producing the anti ICAM-1 Ab was provided
CC by Boehringer Ingelheim Pharmaceuticals Inc. The cells were grown
CC and mRNA isolated and used to prepare cDNA for a library in pSP64
CC vector DNA. The library was grown in E. coli LM1035 and colonies
CC screened using a probe complementary to a sequence in the mouse
CC kappa constant region or with a 980 bp BamHI-EcoRI restriction
CC fragment of a previously isolated mouse IgG2a constant region clone.
CC 10n positive clones were isolated and rescreened. Positive clones

CC from the second round of screening were grown and the DNA inserts
CC sequenced. The protein sequence was deduced from the DNA. The DNA
CC was used to construct humanised Abs having chimeric variable regions,
CC esp. with IgG human constant region domains. The Abs can be used to
CC treat inflammation, to suppress metastasis of haematopoietic tumour
CC cells and growth of ICAM-1 expressing tumour cells, to treat viral
CC infection, to suppress extravascular migration of virally infected
CC leucocytes and to treat asthma.
CC See also R15199.
SQ Sequence 163 AA;
Query Match 75.1%; Score 750; DB 1; Length 163;
Best Local Similarity 70.3%; Pred. No. 9,22e-51;
Matches 97; Conservative 25; Mismatches 13; Indels 3; Gaps 1;
Db 1 MGMSCTFFLVATATGHSQVQLQSGPELVKPGYVKRISKSGSYTFDAIHVKESH 60
QY 1 MGWNCIIFFLVTTATGHSQVQLVQSGAEVKKRPGSSVKVSKASGYTFDYAIQWVRAP 60
DB 61 AKSLKMGIVISAGDTNYNOKFKKATMTVDKSSNTAYLELRLTSEDSATYYCARGGW 120
QY 61 GGGLEWIGIVINITYDNTYNOKFKKATMTVDKSTSTAYMELSSLRSEDTAVYICARAAW 120
Db 121 LLSFDYWGQGTTLTVSS 138
QY 121 YM---DYWGQGTTLTVSS 135
RESULT 11
ID R06369 standard; Protein: 135 AA.
AC R06369;
DT 13-DEC-1990 (first entry)
DE Anti-Tac heavy chain variable region.
KW anti-p55 Tac immunoglobulin (Ig) heavy chain; humanised Ig;
KW Interleukin-2 (IL-2); treatment of T-cell mediated disorders.
FH Key Location/Qualifiers
FT protein 20..135
FT /label=mature heavy chain
FN MO9007861-A.
PN 26-JUL-1990.
PD 28-DEC-1989; U05857.
PR 28-DEC-1989; US-290975.
PR 13-FEB-1989; US-310252.
PA (PROT-) PROTEIN DESIGN LABS.
PI Queen CL, Sellick HE;
DR WPI: 90-253800/33.
DR N-PSDB: Q05600.
PT Chimaeric immunoglobulin(s) blocking IL-2 binding to receptors -
PT comprising human framework and murine complementary determining
PT regions, less immunogenic than murine antibodies
PS Disclosure: P: English.
CC The sequence was prepared based upon a comparison of human antibody
CC EU and human anti-Tac Ab. It is the same as the EU sequence except
CC at certain defined regions. These are CDRs (amino acids 31-35,
CC 50-66 and 99-106), positions at which the EU residue (posn.s 27, 93,
CC 95, 98, 107-109, 111), posn.s immediately adjacent to a CDR of
CC anti-Tac (posn.s 30 and 67) and where the amino acid was thought to
CC have close proximity to the antigen-binding site (posn.s 48-68).
CC Humanised Ig's can bind to IL-2 receptors. They are not significantly
CC immunogenic in humans, are easily and economically produced and
CC have a longer half-life in vivo than murine antibodies. They are
CC useful, optionally attached to a cytotoxic agent, for treatment of
CC T-cell mediated disorders such as graft or transplant rejection.
CC See also Q05601.
SQ Sequence 135 AA;
Query Match 74.9%; Score 748; DB 1; Length 135;
Best Local Similarity 77.8%; Pred. No. 1.35e-50;
Matches 105; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
Db 1 MGMSCTFFLVATATGHSQVQLVQSGAEVKKRPGSSVKVSKASGYTSTRMHVVRAP 60
QY 1 MGWNCIIFFLVTTATGHSQVQLVQSGAEVKKRPGSSVKVSKASGYTSTRMHVVRAP 60


```
OY 1 MGNNCIFFLVTTATGVSQVLQSGAEVKKPGSSVYKSCKASGYFTDYAIQWVROAP 60
Db 61 GGGLEWIGVITNPSTGTEYNOKFRKATITADESTNAYNELSLREDDPAAVYYCARGG 120
OY 61 GGGLEWIGVITNYDNTNMYOKFRKATMTVDKSTAYNELSLREDDPAAVYYCARGG 120
Db 121 VEDYWGQGLTVTVSS 135
OY 121 YMDYWGQGLTVTVSS 135

RESULT 12
ID R29017 standard; Protein: 135 AA.
AC R29017;
DT 30-MAR-1993 (first entry)
DE pUC-RVh-1220d.
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW complementarity determining region; monoclonal; hybridoma; PCR;
KW plasmid; polymerase chain reaction; amplify.
OS Synthetic.
FH Key Location/Qualifiers
FT peptide 1..19 "Leader peptide"
FT region 20..49
FT region /label= FR1
FT region 50..54
FT region /label= CDR1
FT region 55..68
FT region /label= FR2
FT region 69..85
FT region /label= CDR2
FT region 86..117
FT region /label= FR3
FT region 118..124
FT region /label= CDR3
FT region 125..135
FT region /label= FR4

MO9219759-A.
PN 12-NOV-1992.
PF 24-APR-1992: J00544.
PR 25-APR-1991: JP-095476.
PR 19-FEB-1992: JP-032084.
PA (CHUS ) CHUGAI SEIYAKU KR.
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI: 92-398882/48.
DR N-PSDB: Q31391.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure: Page 159-60; 207pp; Japanese.
CC The sequences given in R29016-17 are portions of monoclonal antibodies
CC which were encoded by plasmids contained within the mouse hybridoma,
CC AUK12-20. The DNA encoding the complementarity determining regions
CC (CDR's) was isolated by polymerase chain reaction. These antibodies
CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells
CC were transformed with plasmids containing fragments of the antibody
CC gene which caused the production of the antibody from the hybridoma
CC cell line.
SQ Sequence 135 AA;
```

```
OY 120 YMDYWGQGLTVTVSS 135
Db 120 YMDYWGQGLTVTVSS 135

RESULT 13
ID R29016 standard; Protein: 135 AA.
AC R29016;
DT 30-MAR-1993 (first entry)
DE pUC-RVh-1220d.
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW complementarity determining region; monoclonal; hybridoma; PCR;
KW plasmid; polymerase chain reaction; amplify.
OS Synthetic.
FH Key Location/Qualifiers
FT peptide 1..19 "Leader peptide"
FT region 20..49
FT region /label= FR1
FT region 50..54
FT region /label= CDR1
FT region 55..68
FT region /label= FR2
FT region 69..85
FT region /label= CDR2
FT region 86..117
FT region /label= FR3
FT region 118..124
FT region /label= CDR3
FT region 125..135
FT region /label= FR4

MO9219759-A.
PN 12-NOV-1992.
PF 24-APR-1992: J00544.
PR 25-APR-1991: JP-095476.
PR 19-FEB-1992: JP-032084.
PA (CHUS ) CHUGAI SEIYAKU KR.
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI: 92-398882/48.
DR N-PSDB: Q31391.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure: Page 157-8; 207pp; Japanese.
CC The sequences given in R29016-17 are portions of monoclonal antibodies
CC which were encoded by plasmids contained within the mouse hybridoma,
CC AUK12-20. The DNA encoding the complementarity determining regions
CC (CDR's) was isolated by polymerase chain reaction. These antibodies
CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells
CC were transformed with plasmids containing fragments of the antibody
CC gene which caused the production of the antibody from the hybridoma
CC cell line.
SQ Sequence 135 AA;
```

```
Query Match 74.6%; Score 745; DB 1; Length 135;
Best Local Similarity 74.3%; Pred. No. 2.39e-50;
Matches 101; Conservative 15; Mismatches 18; Indels 2; Gaps 2;
```

Db 1 MDMTRVFCLLAAPGASHQVLQSGAEVKKPGASVYKSCKASGYFTSYIHMVROAP 60
OY 1 MGNNCIFFLVTTATGVSQVLQSGAEVKKPGSSVYKSCKASGYFTDYAIQWVROAP 60
Db 61 GGGLEWIGVITDPFNGSGSYNOKFRGKTYTVDSTNAYNELSLREDDPAAVYYCARGN 120
OY 61 GGGLEWIGVITNYDNTNMYOKFRKATMTVDKSTAYNELSLREDDPAAVYYCARGN 120
Db 121 RF-AYWGQGLTVTVSS 135
OY 120 YMDYWGQGLTVTVSS 135

```
RESULT 14
ID W06442 standard; Protein: 136 AA.
AC W06442;
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 06:22:59 ; Search time 838.43 Seconds
(without alignments)
842.932 Million cell updates/sec

Title: US-09-249-011-7
Perfect score: 396
Sequence: 1 atgagtcacagcagcccaagt.....ggacacaggtggaatacaaa 396

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues
Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_dal: *
2: gb_dal: *
3: gb_on: *
4: gb_ov: *
5: gb_pat: *
6: gb_ph: *
7: gb_pil: *
8: gb_pil: *
9: gb_prl: *
10: gb_prl: *
11: gb_prl: *
12: gb_ro: *
13: gb_sts: *
14: gb_sy: *
15: gb_un: *
16: em_fun: *
17: em_hum1: *
18: em_hum2: *
19: em_in: *
20: em_om: *
21: em_om: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_sy: *
29: em_un: *
30: em_vl: *
31: gb_htg1: *
32: gb_htg2: *
33: gb_in1: *
34: gb_in2: *
35: em_bal: *
36: em_ba2: *
37: em_hum3: *
38: em_hum4: *
39: gb_prl: *
40: gb_htg3: *
41: gb_htg4: *
42: gb_htg5: *
43: gb_htg6: *

44: gb_htg7: *
45: em_htg1: *
46: em_htg2: *
47: em_htg3: *
48: em_hum5: *
49: gb_pil: *
50: gb_prl: *
51: gb_prl: *
52: gb_htg8: *
53: gb_htg9: *
54: gb_htg10: *
55: gb_htg11: *
56: gb_htg12: *
57: gb_htg13: *
58: gb_in3: *
59: gb_htg15: *
60: gb_htg16: *
61: gb_htg17: *
62: em_htg4: *
63: em_htg5: *
64: em_htg6: *
65: em_htg7: *
66: em_hum6: *
67: gb_htg18: *
68: gb_htg19: *
69: gb_htg20: *
70: gb_htg21: *
71: gb_htg22: *
72: gb_htg23: *
73: gb_htg24: *
74: gb_htg25: *
75: gb_htg26: *
76: gb_htg27: *
77: gb_htg28: *
78: gb_htg29: *
79: gb_htg30: *
80: gb_htg31: *
81: gb_vil: *
82: gb_vil2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340	85.9	462	12 M88833	Mus musculus
2	340	85.9	480	5 A13733	A13733 variable re
3	336.2	84.9	406	12 MMU62050	Mus musculus
4	333.6	84.2	419	12 MMU97570	Mus musculus
5	332	83.8	940	5 A44968	A44968 Sequence 24
6	332	83.8	940	5 I64459	I64459 Sequence 24
7	301.4	76.1	401	12 MMLA21LEV	X65774 M. musculus
8	298.2	75.3	402	12 M88833	Mus musculus
9	296	74.7	336	12 AF163745	AF163745 Mus muscu
10	296	74.7	336	12 MDIGKVAR	MDIGKVAR Mus muscu
11	296	74.7	339	12 AB028876	AB028876 Mus muscu
12	295.2	74.5	408	12 S81289	S81289 Igm kappa c
13	295	74.5	339	12 M88833	Mus musculus
14	292.8	73.9	336	12 MDIGKVAL	MDIGKVAL Mus muscu
15	292.8	73.9	336	12 MDIGKVAL	MDIGKVAL Mus muscu
16	288.6	72.9	399	5 A47611	A47611 Sequence 3
17	288.6	72.9	399	5 A80111	A80111 Sequence 3
18	286.4	72.3	336	12 MMU222607	MMU222607 mouse DNA
19	286.4	72.3	337	12 S74056	S74056 Ig VAI-TG2
20	285.4	72.1	439	5 A62621	A62621 Sequence 40
21	285.4	72.1	460	5 A62617	A62617 Sequence 36
22	284.8	71.9	336	12 MMIRACTV	M31353 M. musculus
23	284.8	71.9	336	12 M37022	M37022 Mouse Ig re
24	284.8	71.9	336	12 M37023	M37023 Mouse Ig re

25	284.8	71.9	339	12	MMU60464	U60464 Mus musculu
26	284.4	71.8	336	12	MMU55647	U55647 Mus musculu
27	284.2	71.8	336	12	MMU55674	U55674 Mus musculu
28	283.2	71.5	336	12	MDIGKRAO	Z22060 M.domesticu
29	281.8	71.2	364	12	MMU15982	Y15982 Mus musculu
30	281.4	71.1	336	12	MMU55673	U55673 Mus musculu
31	280.6	70.9	399	12	MMUFABA	M95574 Mus musculu
32	279.8	70.7	411	12	MMIGGVJ5	X02181 M.musculus
33	279.8	70.7	1443	5	AR063210	AR063210 Sequence
34	279	70.5	427	5	A94042	A94042 Sequence 23
35	279	70.5	8068	5	A94046	A94046 Sequence 27
36	278.4	70.3	336	12	MUSIGKADM	M37024 Mouse Ig re
37	278	70.2	336	12	MMU55675	U55675 Mus musculu
38	277.8	70.1	747	14	AC013153	AJ131533 Synthetic
39	277.6	70.1	336	12	MDIGKRAY	Z22023 M.domesticu
40	277.2	70.0	881	12	MUSIGRCLA	L27438 Mouse Immun
41	275.8	69.6	870	5	AR063208	AR063208 Sequence
42	275.4	69.5	375	12	MMIGLCHVJ	X59816 M.musculus
43	274.2	69.2	926	12	RNIGKX3	X16129 Rat mRNA fo
44	274	69.2	330	12	MDIGKVBX	Z22131 M.domesticu
45	273.6	69.1	667	12	MMU62649	U62649 Mus musculu

ALIGNMENTS

```
RESULT 1
MUSIGKPALI LOCUS MUSIGKPALI 462 bp mRNA ROD 18-NOV-1994
DEFINITION Mus musculus Igk chain (anti-Pseudomonas aeruginosa lipoprotein I
antibody) mRNA, 5' end.
ACCESSION M28833.1 GI:576599
VERSION V-segment: anti-lipoprotein antibody; immunoglobulin kappa-chain;
KEYWORDS immunoglobulin light chain.
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) hybridoma CDNA
to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 462)
AUTHORS Margel, M., Eckhardt, A., Ehret, W., von Specht, B. U., Duchene, M. and
Domdey, H.
TITLE Cloning and characterization of cDNAs coding for the heavy and
light chains of a monoclonal antibody specific for Pseudomonas
aeruginosa outer membrane protein I
JOURNAL Gene 74 (2), 335-345 (1988)
COMMENT On Nov 28, 1994 this sequence version replaced gi:342017.
FEATURES
location/Qualifiers
source 1..462
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="Mab 6A4"
/tissue_type="hybridoma"
19..78
/gene="Igk"
CDS
19..>462
/gene="Igk"
/codon_start=1
/product="immunoglobulin kappa chain"
/protein_id="AA53292.1"
/db_xref="GI:576600"
/translation="MDSQAVYILLIWLWSTGCGDIVMSQSPSSLAWSAGEKVTMSCK
SSQSLNSTRKFLAWYQOKGQSPKLLIYASRSGVDPFRFGSGSGDTFTLITIS
SVQADLAVYCKOSYNLRTFGGKRLIKRADAPVTSIFPPSS"
19..462
/gene="Igk"
/mat_peptide
79..>462
/gene="Igk"
/product="immunoglobulin kappa chain"
```

BASE COUNT	114 a	116 c	121 g	111 t		
ORIGIN						
Query Match	85.9%; Score 340; DB 12; Length 462;					
Best Local Similarity	91.2%; Pred. No. 3.9e-107;					
Matches 361; Conservative	0; Mismatches 35; Indels 0; Gaps 0;					
QY	1 atgagctcagagccaggtcttctatgtctgctgctatggtatctgacccgtggtg	60				
DB	19 atgattccacagccccaggtcttctatgtctgctgctatggtatctgacccgtggtg	78				
QY	61 gacatgtctgacacagctcccaagatccctgctgctgtaagtaagagagagccact	120				
DB	79 gacattgtatgtcacagctccatctccctgctgctgctgtaagtaagagagagccact	138				
QY	121 attagctgaatccagctcagctcagctgctgctcagctcagctcagctcagctcagct	180				
DB	139 atgagctgcaaatccagctcagctcagctcagctcagctcagctcagctcagctcagct	198				
QY	181 tggctacacagagaaacacagagcagctcctaaactgctgctatctggtgacatccactag	240				
DB	199 tggctacacagagaaacacagagcagctcctaaactgctgctatctggtgacatccactag	258				
QY	241 gaatctggagtcctctgctcagctcagctcagctcagctcagctcagctcagctcagctc	300				
DB	259 gaatctggagtcctctgctcagctcagctcagctcagctcagctcagctcagctcagctc	318				
QY	301 atcagcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagct	360				
DB	319 atcagcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagct	378				
QY	361 tacacgcttcgacagagggagagagagagagagagagagagagagagagagagagag	396				
DB	379 cggacgttcgctggagagcaccacagctggaaatcaaa	414				
RESULT 2						
LOCUS	A13733	480 bp	DNA	PAT 03-JAN-1994		
DEFINITION	variable region of a monoclonal antibody which cross reacts with 19 known P.aeruginosa serotypes.					
ACCESSION	A13733					
VERSION	A13733.1	GI:491741				
KEYWORDS	synthetic construct.					
SOURCE	synthetic construct.					
ORGANISM	artificial sequence.					
REFERENCE	1 (bases 1 to 480)					
AUTHORS	Domdey, H., Margel, M. and von Specht, B. U.					
TITLE	Monoclonal antibodies to Pseudomonas aeruginosa, their production and use					
JOURNAL	Patent: EP 038395-A 1 25-OCT-1989;					
BEHRINGERWERKE Aktiengesellschaft						
FEATURES	Location/Qualifiers					
source	1..480					
CDS	/organism="synthetic construct"					
	/db_xref="taxon:32630"					
	37..>480					
	/codon_start=1					
	/transl_table=11					
BASE COUNT	with 19 P.aeruginosa serotypes"					
	/protein_id="CAA01126.1"					
	/db_xref="GI:491742"					
	/translation="MDSQAVYILLIWLWSTGCGDIVMSQSPSSLAWSAGEKVTMSCK					
	SSQSLNSTRKFLAWYQOKGQSPKLLIYASRSGVDPFRFGSGSGDTFTLITIS					
ORIGIN	SVQADLAVYCKOSYNLRTFGGKRLIKRADAPVTSIFPPCE"					
	115 a					
	117 c					
	136 g					
	112 t					
Query Match	85.9%; Score 340; DB 5; Length 480;					

Best Local Similarity 91.2%; Pred. No. 3.9e-107;
Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atggaatcaagagccaggtctctatattctgctctgtagtgatctgacactgtgg 60
DB 37 ATGATTTCAAGGCCGCGGTTCTATATGCTCTGCTATGCTGATCTGATCTGCTGG 96
QY 61 gacatgtgtgacagagctccagattccctgctgtaagcttagagagagggccact 120
DB 97 GACATTTGATGTCACAGTCTCCATCTCCCTGCTGTGTCAGACAGAGAAAGGTCCT 156
QY 121 atagatgcaaatccagctcagctcagctcagctcagctcagctcagctcagctc 180
DB 157 ATGAGCTGCAATCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 216
QY 181 tggtaacagagaaacag 240
DB 217 TGGTACACAGAGAAACAGGAGCACTCTAACTGCTGATCTGCTGCTGCTGCTGCT 276
QY 241 gaatctggagctccctgctcagctcagctcagctcagctcagctcagctcagctc 300
DB 277 GAATCTGGGCTCCCTGATCTGCTCTACAGGAGAGTGGATCTGGAGAGATTTACTCTCACC 336
QY 301 atcagcagctcagcagctcagcagctcagcagctcagcagctcagcagctcagcag 360
DB 337 ATCAGCAGTGTGACAGGCTGAAGACCTGGAGATTTATTACTGCAAGCAATCTTATATCTT 396
QY 361 tacagcttgagcag 396
DB 397 CGGACGTTGCTGGAGGACCAAGCTGGAATCAAA 432

RESULT 3

LOCUS MMU62050 406 bp mRNA ROD 19-FEB-1997
DEFINITION Mus musculus polyreactive autoantibody, immunoglobulin light chain
ACCESSION U62050
VERSION U62050.1 GI:1438580
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 406)
Diaw, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P. M. and
Dighiero, G.

TITLE Structural and affinity studies of IgM polyreactive natural
JOURNAL J. Immunol. 158 (2), 968-976 (1997)
MEDLINE 97146071
REFERENCE 2 (bases 1 to 406)
AUTHORS Diaw, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P. M. and
Dighiero, G.

TITLE Direct Submission
JOURNAL Submitted (25-JUN-1996) Laboratoire d'Immunohematologie et
d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris
75724 Paris Cedex 15, France
FEATURES
source location/Qualifiers

1. .406
/organism="Mus musculus"
/strain="(CBA/NXBALB/c)F1"
/db_xref="taxon:10090"
/sex="male"
/note="hybridoma M25-9; 6-day-old spleen cells fused with
SP2/0 myeloma cells"
<1. .>406
/codon_start=1
/product="polyreactive autoantibody, immunoglobulin light
chain kappa"
/protein_id="AAB47613.1"
/db_xref="GI:1438581"
/translation="QVLLILLMWSTGCDIYVSGSPSLAVSAGEKVTMSCKSSQSL

CDS

1. .406
/organism="Mus musculus"
/strain="(CBA/NXBALB/c)F1"
/db_xref="taxon:10090"
/sex="male"
/note="hybridoma M25-9; 6-day-old spleen cells fused with
SP2/0 myeloma cells"
<1. .>406
/codon_start=1
/product="polyreactive autoantibody, immunoglobulin light
chain kappa"
/protein_id="AAB47613.1"
/db_xref="GI:1438581"
/translation="QVLLILLMWSTGCDIYVSGSPSLAVSAGEKVTMSCKSSQSL

BASE COUNT 101 a 99 c 108 g 98 t
ORIGIN
INSRTKRYLAMYQAKPGOSPKLLIYMAS*RESGVDPDRFTSGSGSTDTLLTSSVOAE
DLAVYCKOSYNLYTEGGTKLEIKRADAPV"

Query Match 84.9%; Score 336.2; DB 12; Length 406;
Best Local Similarity 92.7%; Pred. No. 8e-106;
Matches 353; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 16 caggtctctatattgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 75
DB 1 CAGGTCTTATATGCGTCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 76 cagctccagaattccctgctgtgaagcttagagagagagagagagagagagagagagag 135
DB 61 CAGCTCTCAATCTCCCGGCTGTGTGTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 136 agtcaagctctgctcacaagtagaaccgagagagagagagagagagagagagagagag 195
DB 121 AGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGACTACTTGCTTGGTGTACACAGAGAA 180
QY 196 ccaaggagagccctcctaactgctgctgctgctgctgctgctgctgctgctgctgct 255
DB 181 CCAGGCGAGTCTCCTTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 256 gatcgctcagtgagcagtgatctggtgacagattcactcactcactcactcactcactcag 315
DB 241 GATGCTTCAAGGACAGTGTGAGACAGATTTACTCTCAGCAGCAGCAGCAGCAGCAGCAG 300
QY 316 gctgaagacgtgagcttattactgacagcagcagcagcagcagcagcagcagcagcag 375
DB 301 GCTGAAGACCTGCGAGCTTATTACTGCAAGCAATCTTATTCTGTACACCTTGGAGGG 360
QY 376 gggacccaaggtggaataaaa 396
DB 361 GGGACCAAGCTGGAGATAAAA 381

RESULT 4

LOCUS MMU97570 419 bp mRNA ROD 11-JUN-1997
DEFINITION Mus musculus immunoglobulin light chain variable region (IgK) mRNA,
partial cds.
ACCESSION U97570
VERSION U97570.1 GI:2183076
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 419)
Feijó, G. C. S., Sabbaga, J., Carneiro, C. R. W. and Brigido, M. M.

TITLE Variable region structure and staphylococcal protein A binding
JOURNAL Immunology (1997) in press
REFERENCE 2 (bases 1 to 419)
AUTHORS Brigido, M. M.
JOURNAL Direct Submission
Submitted (15-APR-1997) Biologia Celular, Universidade de Brasília,
Campus Universitario, Asa Norte, Brasília, DF 70910-900, Brazil
FEATURES
source location/Qualifiers

1. .419
/organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
/cell_line="1H12"
/cell_type="hybridoma"
1. .>419
/gene="Igk"
21. .>419
/gene="Igk"
/note="rearranged Vk8 to Jk1 region"

CDS

gene
1. .>419
/gene="Igk"
21. .>419
/gene="Igk"
/note="rearranged Vk8 to Jk1 region"

/codon_start=1
/product="Immunoglobulin light chain variable region"
/protein_id="AAB60862.1"
/db_xref="GI:2183077"
/translation="MDSQAVYILLLVSGTCDITNSQSPSLAVAGEKWTMSCK
SSQSLKSRTRNYLAWYQKRGQSPKLLIYAWYRESGVDPDRFGSGSDFTLLTIS
SVQADLAIYCKQSYNLRTFGSGPKLEIKR"
BASE COUNT 105 a 101 c 115 g 98 t
ORIGIN

Query Match 84.2%; Score 333.6; DB 12; Length 419;
Best Local Similarity 90.2%; Pred. No. 6.5e-105;
Matches 357; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 atgagttcagagccaggttcttatatgtcgtcgtatgtgtatcgtgcacctgtgg 60
|||||
DB 21 ATGGATTACAGGCCAGGTTCTTATATGCTGCTGCTATGGGTATGCTGACCTGTGG 80
QY 61 gacattgtctacacagctcccaagctccctgtcttaagcttaagagagagggccact 120
|||||
DB 81 GACATTGTATGTACAGCTCTCCATCTCTCGCTGTGTGTCAGCAGGAGAGAGAGTCACT 140
QY 121 attaagctgaatcccaagtcagagctgtctcaacagtagaacccgagagactatgtgt 180
|||||
DB 141 ATGAGCTGCAAGTCCAGTCAAGATGCTCAAAAGTAGAACCCGAGAGATTACTTGCTT 200
QY 181 tggtaaccagagaaccagagcgagcctcctaaactctatctactgtggcatccactagg 240
|||||
DB 201 TGGTACCAAGCAAAACAGGAGAGTCTCCAAACCTGCTATCTACAGGCAATCCACTAGG 260
QY 241 gaatctgggtccctgagctcagctcagtgagtgagtcgtggagacagattcactccacc 300
|||||
DB 261 GAATCTGGGGTCCCTGATGCTTTCACAGGCACTGGATCTGGGACAGATTTCACCTCACC 320
QY 301 atcagcagctctgcaggtctgaagacgttgcagttatctactgcagcaactataatctt 360
|||||
DB 321 ATCAGCAGTGTGACAGCTGAAGACCTGGCAATTATTACTGCAAGCAATCTATATCTT 380
QY 361 tacagcttcgagcagggagaccaaagtggaaataaaa 396
|||||
DB 381 CGGACGTTGCTGGTAGAGGCCCAAGCTGGAATCAAA 416

RESULT 5
A44968 940 bp DNA PAT 07-MAR-1997
LOCUS A44968
DEFINITION Sequence 24 from Patent W09515382.
ACCESSION A44968
VERSION A44968.1 GI:2299554
KEYWORDS
SOURCE
ORGANISM
unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 940)
Rose, M.S., Boot, C., Copley, C.G., Paterson, D.S., Hall, S.M.,
Wright, A.F. and Blakey, D.C.
TITLE BINDING STRUCTURES DIRECTED AGAINST THE CA55.1 ANTIGEN
JOURNAL Patent: WO 9515382-A 24 08-JUN-1995;
ZENECA LTD (GB)
COMMENT Other publication GB 2297751 960814
Other publication CA 2174972 950608
Other publication CA 9409266 950605
Other publication AU 1113095 950619.
FEATURES
source
1..940
/organism="unclassified"
/db_xref="taxon:32644"

BASE COUNT 241 a 266 c 213 g 220 t
ORIGIN

Query Match

83.8%; Score 332; DB 5; Length 940;

Best Local Similarity 89.9%; Pred. No. 2.6e-104;
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 atgagttcagagccaggttcttatatgtcgtcgtatgtgtatcgtgcacctgtgg 60
|||||
DB 10 ATGGATTACAGGCCAGGTTCTTATATGCTGCTGCTATGGGTATGCTGACCTGTGG 69
QY 61 gacattgtctacacagctcccaagctccctgtcttaagcttaagagagagggccact 120
|||||
DB 70 GACATTGTATGTACAGCTCTCCATCTCTCGCTGTGTGTCAGCAGGAGAGAGTCACT 129
QY 121 attaagctgaatcccaagtcagagctgtctcaacagtagaacccgagagactatgtgt 180
|||||
DB 130 ATGAGCTGCAAGTCCAGTCAAGTCTCTCCATCAAGTAGAACCCGAGAGATTACTTGCT 189
QY 181 tggtaaccagagaaccagagcgagcctcctaaactctatctactgtggcatccactagg 240
|||||
DB 190 TGGTACCAAGCAAAACAGGAGAGTCTCCAAACCTGCTATCTATGAGGCAATCCACTAGG 249
QY 241 gaatctgggtccctgagctcagctcagtgagtgagtcgtggagacagattcactccacc 300
|||||
DB 250 ACATCTGGGGTCCCTGATGCTTTCACAGGCACTGGATCTGGGACAGATTTCACCTCACC 309
QY 301 atcagcagctctgcaggtctgaagacgttgcagttatctactgcagcaactataatctt 360
|||||
DB 310 ATCAGCAGTGTGACAGCTGAAGACCTGGCAATTATTACTGCAAGCAATCTATATCTT 369
QY 361 tacagcttcgagcagggagaccaaagtggaaataaaa 396
|||||
DB 370 CGGACGTTGCTGGTAGAGGCCCAAGCTGGAATCAAA 405

RESULT 6
I64459 940 bp DNA PAT 07-OCT-1997
LOCUS I64459
DEFINITION Sequence 24 from patent US 5665357.
ACCESSION I64459
VERSION I64459.1 GI:2481353
KEYWORDS
SOURCE
ORGANISM
Unknown.
unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 940)
Rose, M.S., Boot, C., Copley, C.G., Paterson, D.S., Stephen,
Hall, S.M., Margaret, Wright, A.F., Firman and Blakey, D. Charles.
TITLE Antibodies recognizing tumor associated antigen CA 55.1
JOURNAL Patent: US 5665357-A 24 09-SEP-1997;
LOCATION/Qualifiers
source
1..940
/organism="unknown"

BASE COUNT 241 a 266 c 213 g 220 t
ORIGIN

Query Match 83.8%; Score 332; DB 5; Length 940;
Best Local Similarity 89.9%; Pred. No. 2.6e-104;
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 atgagttcagagccaggttcttatatgtcgtcgtatgtgtatcgtgcacctgtgg 60
|||||
DB 10 ATGGATTACAGGCCAGGTTCTTATATGCTGCTGCTATGGGTATGCTGACCTGTGG 69
QY 61 gacattgtctacacagctcccaagctccctgtcttaagcttaagagagagggccact 120
|||||
DB 70 GACATTGTATGTACAGCTCTCCATCTCTCGCTGTGTGTCAGCAGGAGAGAGTCACT 129
QY 121 attaagctgaatcccaagtcagagctgtctcaacagtagaacccgagagactatgtgt 180
|||||
DB 130 ATGAGCTGCAAGTCCAGTCAAGTCTCTCCATCAAGTAGAACCCGAGAGATTACTTGCT 189
QY 181 tggtaaccagagaaccagagcgagcctcctaaactctatctactgtggcatccactagg 240
|||||
DB 190 TGGTACCAAGCAAAACAGGAGAGTCTCCAAACCTGCTATCTATGAGGCAATCCACTAGG 249

```

QY 241 gaatctgggtccctgatactcagctgagcagtgatctggagacattcactcacc 300
    |||||||
DB 250 ACATCTGGGGCCCTGATCGCTTCACAGGCGATGATCTGGGACAGATTACTCTCACC 309
    |||||||

QY 301 atcagcagctcagcagctgaaagacgtgacagttatctactcagcgaattctatactt 360
    |||||||
DB 310 ATCAGCAGTGTGAGAGGCTGGAAGACCTGACATTTATTACTCAGACGATCTTATCTCTT 369
    |||||||

QY 361 tacacgttcggacagagggaccaggttggaataaaa 396
    |||||||
DB 370 CGGACGTTGGGTGGAGCCACCAGCTGGAATCAAA 405
    |||||||

RESULT 7
MMLA2JILEV 401 bp DNA ROD 15-JUN-1993
LOCUS M.musculus DNA for Ige antibody light chain (VJ).
DEFINITION X65774
ACCESSION X65774.1 GI:312076
VERSION Ige antibody; J-segment; light chain; V-region.
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Kofler,H., Schnegg,I., Geley,S., Helmlberg,A., Varga,J.M. and
AUTHORS Kofler,R.
TITLE Mechanism of allergic cross-reactions--III. cDNA cloning and
JOURNAL variable-region sequence analysis of two Ige antibodies specific
MEDLINE for trinitrophenyl
FEATURES Mol. Immunol. 29 (2), 161-166 (1992)
Source 92178225
Location/Qualifiers
1. .401
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="IGEL42 (ATCC-TIB142)"
3. .>401
/codon_start=1
/product="Ige antibody light chain (VJ)"
/protein_id="CAA658.1"
/db_xref="GI:312077"
/translation="MDSQAYVLMILLMWSGTCGDYMSQSPSLAVSVEKXTMSCK
SOSLIYSSNQKNTLAWYQKPGQSPKLLIYMASTRSGVPDRFTSGSGTDFTLTIS
SVRAEDLAVYTCQYINPSTFGGTYLEIK"
3. .>401
V-region
/product="Ige antibody light chain (VJ)"
sig_peptide 3. .62
J_segment 365. .>401
BASE COUNT 100 a 91 c 105 g 105 t
ORIGIN
Query Match 76.1%; Score 301.4; DB 12; Length 401;
Best Local Similarity 86.5%; Pred. No. 1e-93; Indels 3; Gaps 1;
Matches 345; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 1 atgattcacagcgccaggtctctatatctgctgctgctatgctgacacgtgagg 60
    |||||||
DB 3 ATGATTCACAGGCCGCGAGTCTTATGTTACTGCTGCTATGGTATCTGTGATCCCTGTGG 62
    |||||||

QY 61 gacattgtcgtacacagctccagatccctgctgctgaagcttaaggagagggccact 120
    |||||||
DB 63 GACATTGTGATGTACAGTCTCCATCTCCTAGCTGTGTCAGTTGGAGAGAGGTTACT 122
    |||||||

QY 121 attagctgcaaatccagctcaagctcgtctcaagctagaaccggagaaactcttgct 180
    |||||||
DB 123 ATGAGCTGCAGAGTCAGTCAAGCCTTTTATATATGATACCAATCAAAAGACTTGGCC 182
    |||||||

QY 181 tggatcacagcagaacacagcgccctcctctaactgctgactctactggtgacatccactag 240
    |||||||
DB 183 TGGTACACGCGGAACACGAGCGGCGAGTCTCTTAAGTGTGATTTACTGGCATCCACTAGG 242
    |||||||

```

```

QY 241 gaatctgggtccctgatactcagctgagcagtgatctggagacattcactcacc 300
    |||||||
DB 243 GAATCTGGGGCCCTGATCGCTTCACAGGCGATGATCTGGGACAGATTACTCTCACC 302
    |||||||

QY 301 atcagcagctcagcagctgaaagacgtgacagttatctactcagcgaattctatactt 357
    |||||||
DB 303 ATCAGCAGTGTGAGAGGCTGGAAGACCTGACATTTATTACTGTCAGCATTTATATAGCTCT 362
    |||||||

QY 358 cttaacagcttcggacagagggaccaggttggaataaaa 396
    |||||||
DB 363 CCGTACAGTTCGAGGAGGGGACCAGCTGGAATATAAA 401
    |||||||

RESULT 8
MUSIGKALA 402 bp mRNA ROD 14-JUL-1993
LOCUS Mouse Ig rearranged K-chain mRNA V-region, 5' end.
DEFINITION M98042
ACCESSION M98042.1 GI:196749
VERSION V-region; hepatitis; immunoglobulin light chain; processed gene.
KEYWORDS Mus musculus (strain BALB/c, sub-species domesticus) spleen cDNA to
SOURCE mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
REFERENCE Hong,H.J., Kim,A.K., Ryu,C.J., Park,S.S., Chung,H.K., Kwon,K.S.,
AUTHORS Kim,K.L., Kim,J. and Han,M.
TITLE Cloning and characterization of cDNA's coding for heavy and light
JOURNAL chains of a monoclonal antibody specific for pre-S2 antigen of
MEDLINE hepatitis B virus
FEATURES Gene 121, 331-335 (1992)
Source 93077049
Location/Qualifiers
1. .402
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="H8"
/cell_type="hybridoma"
/tissue_type="spleen"
/map="Chromosome 6"
1. .60
sig_peptide 1. .402
CDS 1. .402
/codon_start=1
/function="specific for pre-S2 antigen of hepatitis B
virus"
/product="immunoglobulin kappa-chain"
/protein_id="AAA38777.1"
/db_xref="GI:196750"
/translation="MDSQAYVLMILLMWSGTCGDYMSQSPSLAVSVEKXTMSCK
SOSLIYSSNQKNTLAWYQKPGQSPKLLIYMASTRSGVPDRFTSGSGTDFTLTIS
SVRAEDLAVYTCQYINPSTFGGTYLEIK"
61. .402
mat_peptide 61. .402
BASE COUNT 102 a 93 c 100 g 107 t
ORIGIN
Query Match 75.3%; Score 298.2; DB 12; Length 402;
Best Local Similarity 86.0%; Pred. No. 1.3e-92;
Matches 343; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

QY 1 atgattcacagcgccaggtctctatatctgctgctgctatgctgagctatctgacactgagg 60
    |||||||
DB 1 ATGATTCACAGGCCGCGAGTCTTATGTTACTGCTGCTATGGTATCTGTGATCCCTGTGG 60
    |||||||

QY 61 gacattgtcgtacacagctccagatccctgctgctgaagcttaaggagagggccact 120
    |||||||
DB 61 GACATTGTGATGTACAGTCTCCATCTCCTAGCTGTGTCAGTTGGAGAGAGGTTACT 120
    |||||||

```

Cy	121	atgactcgaatccagctcagctcagctcgaacagctagaaccgcgaggaactctgct	180
Pb	121	atgactcgaactccagctcagctcagctcgaacagctagaaccgcgaggaactctgct	180
Cy	181	tgtaccagcagaaccagggcagcctccctaaactcgtatctactctggcaltcactag	240
Pb	181	tgtgTCCAGCAGCAAAACCAGGGCGAGTCTCTTAACTCGTATTACTGGGCATCCACTAGG	240
Cy	241	gaactcggggtccctcgatcgctcagctcagctgagcaatgagatctcgggaagattcactaac	300
Pb	241	GAATCTGGGGTCCCTGATCGCTTCAACAGGCACTGATCTGAGACAGATTTCCTCTCAC	300
Cy	301	atcagcagctcgtcagagcttgaagacgctggcagttatctactgcagcaactctata--at	357
Pb	301	ATCAGCAATGTGAAGCGCTGAAGACCTCGGACGATTCTTACTGTACACCAATATTATAACTAT	360
Cy	358	ctttacacgcttcggacaggggacgaagtggtggaataaaa	396
Pb	361	CGGTCCAGCTTGGAGGGGACCTPACCTCGGAAATAAAA	399

RESULT	9
AF163745	
LOCUS	AF163745 336 bp mRNA
DEFINITION	Mus musculus mab 27.4.1 immunoglobulin light chain variable region
VERSION	AF163745 partial cds.
ACCESSION	AF163745
KEYWORDS	house mouse.
SOURCE	GI:5690296

REFERENCE	1 (bases 1 to 336)
AUTHORS	Wenters, N. M., Galvin, J. E., Adderson, E. E. and Cunningham, M. W.
TITLE	Molecular Analysis of Crossreactive Anti-myosin/Anti-Streptococcal Mouse Monoclonal Antibodies
JOURNAL	unpublished
REFERENCE	2 (bases 1 to 336)
AUTHORS	Wenters, N. M. and Cunningham, M. W.
TITLE	Direct Submission
JOURNAL	Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma

FEATURES	Location/Qualifiers
source	1. .336

CDS

```

/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/note="mab 27.4.1"
<1..>336
/feature="V-J segments"
/codon_start=1
/product="immunoglobulin light chain variable region"
/protein_id="AAd7024.1"
/db_xref="GI:5690297"
/translation="DIYMSGSPSSLAVSAGEKVTYMSCKSSQSLMSFRKNTLMTYQQ
KPGSGPLLIYMTSTRESGVDPFRFTSGSGCTPTLTITSSVQAEADLAVYCKQSYLNTY
GGGCTKLEIR"

```

BASE COUNT	91 a	83 c	86 g	76 t
ORIGIN				

Query Match	74.7%	Score 296:	DB 12:	Length 336:
Best Local Similarity	92.6%	Pred. No. 7.5e-92:		
Matches 311; Conservative	0;	Mismatches 25;	Indels 0;	Gaps 0;

Oy 61 gacattgtcgtgacacaagctctccagatcccctgcgtgtaagctaaggagaagggccact 120
||||||| ||||| ||||| ||||| |||||
Db 1 GACATTGTGATGTCAAGTCTCCCATCCTCCCCTGGCTGTGTCAAGCAGGAGAAGACTACT 60

QY 121 attagctgcaaatccagtcagagtcctgctcaacagtagaacccgagagaactacttgct 180

Db	61	ATGAGCTCAATATCAGTCAAGTCTGCTCAACAGTGAACCCGAAAGACTACTTGCT	120
Oy	181	tgfraccagcagaaacacagggcagccctcctaactggtatctactgtagatcacagg	240
Db	121	TGTRACAGCGAANAACAGGSCATCTCTTAACTGCTGATCTTACTGCGCATCCACTAGG	180
Oy	241	gaatctggggtccctgatcgccttcagttgcagtgatctcggacagatctcaactcac	300
Db	181	GAATCTGGGGTCCCTGATCAGCGTTTACAGGCGAGTGGATCTGGGAGATTTCACTCTCACC	240
Oy	301	atccagcagctcgcagggcgtcgaagacgtitgacgtttattactgcacgcacatcttaactc	360
Db	241	ATCAGCACTGTGCAGCGCTGAGACCTGGCACTTATATCTGCAAGCAATCTTATAACTCG	300
Oy	361	tacacgttcgcagcaggggacccaagtgtagaataaa	396
Db	301	TACAGCTTCGAGGGGGGACCAACTGGAATAATAAA	336

RESULT	10			
MDIGKVAR				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
	MDIGKVAR	336 bp	mRNA	ROD
	M.domesticus	Igk variable region.		
	Z22063			
	Z22063.1	GI:297629		
	anti-DNA antibody; Igk gene; Igk variable region; Immunoglobulin western European house mouse.			

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE
1 (bases 1 to 336)	Tillman, D.M.,	Jou, N.T., Hill, R.J. and Matton, T.N.			
	Both IgM and IgG anti-DNA antibodies are the products of clonally				
	selective B cell stimulation in (NZB x NZW)F1 mice				
	J. Exp. Med.	176 (3), 761-779 (1992)			
9238144					
2 (bases 1 to 336)					

AUTHORS
TITLE
JOURNAL

FEATURES	Location/Qualifiers
source	1. .336

```

/organism="Mus musculus domesticus"
/strain="(NZB x NZW)F1"
/isolate="mouse #165"
/db_xref="taxon:10092"
/chromosome="6"
/sex="Female"
/dev_stage="somatic variant"
/tissue_type="spleen"
/cell_type="hybridoma"
/cell_line="165.45"
1. | 336
/gene="Igf"
<1. | >336

```

```

/function="pappa light chain variable region for anti-DNA
antibody: VK8 family"
/codon_start=1
/product="immunoglobulin variable region"
/protein_id="CAA8037.1"
/db_xref="GI:287630"
/translation="DIWMSQSPSLAVAGAGKVTWMSCKSSOSLINTKNTKNTLAATG
KPGQSKRLIIYMASTRSGVDPDRFTGSSGSDFTLTITSSVAQEDLAVYICKOSINILY
FGGGRLEIK"

```

Query Match	74.78; Score 296; DB 12; Length 336;
-------------	--------------------------------------

Best Local Similarity 92.6%; Pred. No. 7.5e-92;
Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 61 gacattgctgacacacatccatccatccctgctgctgtaagcttagagagagggccact 120
|||||
Db 1 GACATTGTAAGTGCACAGCTCCATCCCTCCGCTGTGTGACAGGAGAGAGTCTACT 60
|||||

QY 121 attactcaatccagtcagagctgtctcaacagtagaaccgagagaaacttggct 180
|||||
Db 61 ATGAGCTCAAAATCCAGTCAGAGTGTCTCAACAGTAGAACCCGAAAGACTACTTGGCT 120
|||||

QY 181 tggtaaccagaaaccagggcagcctcttaactgctgatacttagggcatccactagg 240
|||||
Db 121 TGGTACAGCAAGAAACAGGCGAGTCTCCTTAACGCTGATCTACTGGGCATCCACTAGG 180
|||||

QY 241 gaattgggtccctgactgctgctcagtgagtgatctggagacatttcacttcacc 300
|||||
Db 181 GAATCTGGGGTCCCTGATCGCTTCACAGGACGTGATCTGGGACAGATTTCACCTCCACC 240
|||||

QY 301 atcagcagctcgcagcgcgaagcgttgagttacttactgacgcaatcttatactt 360
|||||
Db 241 ATCAGCATGTGTCAGGCTGGAAGACCTGGCAGTTTATTCTGCAAGCAATCTTATATCTG 300
|||||

QY 361 tacacgttcgcagcagggacccaaggtggaataaaa 396
|||||
Db 301 TACACGTTGCGAGGGGGGACCAAGCTGGAATATAAA 336
|||||

RESULT 11
AB028876 339 bp mRNA ROD 07-DEC-1999
LOCUS Mus musculus mRNA for 5.2 IgG light chain (variable region),
DEFINITION partial cds.
AB028876
ACCESSION AB028876.1 GI:5103290
VERSION 5.2
KEYWORDS 5.2 IgG light chain variable region.
SOURCE Mus musculus cell_line:hybridoma 5.2 cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
Yoshida,S., Matsuoaka,H., Luo,E., Iwai,K., Arai,M., Sinden,R.E. and
Ishii,A.
TITLE A single-chain antibody fragment specific for the Plasmodium
berghei ookinete protein Pbs21 confers transmission blockade in the
mosquito midgut
Wol. Biochem. Parasitol. 104 (2), 195-204 (1999)
20058748
2 (bases 1 to 339)
Yoshida,S.
DIRECT SUBMISSION
SUBMITTED (11-JUN-1999) to the DDBJ/EMBL/GenBank databases. Shigeto
Yoshida, Dichi Medical School, Department of Medical Zoology;
Yakushiji 3311-1, Minamikawachimachi, Tochiy 329-0498, Japan
(E-mail:shigetoejichi.ac.jp, Tel:81-285-58-7339,
Fax:81-285-44-6489)
FEATURES
source
1..339
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="hybridoma 5.2"
1..339
/gene="5.2 VL"
<1..>339
/gene="5.2 VL"
/note="light chain variable region of 5.2 monoclonal
antibody"
/codon_start=1
/product="5.2 IgG light chain"
/protein_id="BAI78904.1"
/db_xref="GI:5103291"
/translation="DIWVSQPSLAVSAGEKVTMSCKSSQSLNSRTRKRYLAWYQO
KPGQSPKLITWASTRESGVDRFTGSGSDFTLTISVQAEIDLAVYCKQSYNLVT

BASE COUNT 92 a 84 c 87 g 76 t
ORIGIN
FGGCTKLEIKO"
Query Match 74.7%; Score 296; DB 12; Length 339;
Best Local Similarity 92.6%; Pred. No. 7.5e-92;
Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 61 gacattgctgacacacatccatccatccctgctgctgtaagcttagagagagggccact 120
|||||
Db 1 GACATTGTAAGTGCACAGCTCCATCCCTCCGCTGTGTGACAGGAGAGAGTCTACT 60
|||||

QY 121 attactcaatccagtcagagctgtctcaacagtagaaccgagagaaacttggct 180
|||||
Db 61 ATGAGCTCAAAATCCAGTCAGAGTGTCTCAACAGTAGAACCCGAAAGACTACTTGGCT 120
|||||

QY 181 tggtaaccagaaaccagggcagcctcttaactgctgatacttagggcatccactagg 240
|||||
Db 121 TGGTACAGCAAGAAACAGGCGAGTCTCCTTAACGCTGATCTACTGGGCATCCACTAGG 180
|||||

QY 241 gaattgggtccctgactgctgctcagtgagtgatctggagacatttcacttcacc 300
|||||
Db 181 GAATCTGGGGTCCCTGATCGCTTCACAGGACGTGATCTGGGACAGATTTCACCTCCACC 240
|||||

QY 301 atcagcagctcgcagcgcgaagcgttgagttacttactgacgcaatcttatactt 360
|||||
Db 241 ATCAGCATGTGTCAGGCTGGAAGACCTGGCAGTTTATTCTGCAAGCAATCTTATATCTG 300
|||||

QY 361 tacacgttcgcagcagggacccaaggtggaataaaa 396
|||||
Db 301 TACACGTTGCGAGGGGGGACCAAGCTGGAATATAAA 336
|||||

RESULT 12
S81289 408 bp mRNA ROD 23-MAY-1996
LOCUS IGM kappa chain variable region {CDRL1 to CDR3 region} [rats, LEW,
DEFINITION HAR-1 hybridoma cells, mRNA Partial, 408 nt].
S81289
ACCESSION S81289.1 GI:1326409
VERSION 1
KEYWORDS 5.2 IgG light chain variable region.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 408)
Borje,D.C., Cramer,D.V., Shirwan,H., Wu,G.D., Rodriguez,O.,
Chapman,F.A. and Makowka,L.
TITLE Genetic control of the humoral immune response to xenografts. II.
Monoclonal antibodies that cause rejection of heart xenografts are
encoded by germline immunoglobulin genes
Transplantation 60 (12), 1504-1510 (1995)
96125839
JOURNAL GenBank staff at the National Library of Medicine created this
MEDLINE entry (NCBI gisbq 176405) from the original journal article.
REMARK This sequence comes from Fig. 4.
FEATURES
source
1..408
/organism="Rattus sp."
/db_xref="taxon:10118"
7..408
/partial
/gene="IgM kappa chain variable region"
7..408
/partial
/gene="IgM kappa chain variable region"
/note="IgM kappa chain variable region"
/note="hamster heart xenograft rejection-associated";
This sequence comes from Fig. 4"
/codon_start=1
/product="IgM kappa chain variable region"
/protein_id="AA835891.1"
/db_xref="GI:1326410"

```

/translation="MESQTVLMSLLLVSGTDIVMTQTPSSQANVASAEKYMISCK
SSSLLYNENKNYLAWYQKPGOSPILLIWTASTREGVDPREIGSSGTDFTLTIS
SVAQEDLAVYYCCQYINLYTFGAGTKLELKA"
BASE COUNT      106 a      108 g      94 t
ORIGIN

```

Query Match	74.5%;	Score 295.2;	DB 12;	Length 408;
Best Local Similarity	84.1%;	Pred. No. 1.5e-91;		
Matches 333;	Conservative 0;	Mismatches 63;	Indels 0;	Gaps 0;

QY	1	atggtctcaagggcccaaggtctcttataatgctgcgtcctaaggtaactctgcaacctgtgg	60
Db	7	ATGGAAATCAACAGACACAGAGTCTCTCATGTGCCCTGCTGCTCTGGGATCTGTACCTGTGGG	66
QY	61	gacattctgctgacacagctctccagattccctgctgctgtaagcttaggaagagggccact	120
Db	67	GACATTGTGGATATACCCAGACTCCATTCCTCCAGGGGCTGTCCAGCAGGGGAGAAAGTCACT	126
QY	121	attagctgcaaatccacgtacagatcgtctcaacagtagaaccgagagaactacttgcct	180
Db	127	ATGAGCTGCACATCCAGATCAGAGCTTTTATTCACATGAAMAAAAAGAACTACTGTGGCC	186
QY	181	tgtrtcccgacgaagaaaccaggagcagctccctaactgctgtaacttactgagcatccactagg	240
Db	187	TGGTACCGACAAACCCAGGGCAAGTCTCTTAACCTGCTATCTACTGCGGCATCCACTAAG	246
QY	241	gaatctggaggtccctcgatcgtctcaagtgtgcagtgtactcggagcaagattcaactccacc	300
Db	247	GAATCTGGGGTCCCTGATGCTTCATATAGGCAATGGATCTGGGACAGATTTCACTCTGACC	306
QY	301	atcagcagctctgcagagcttgaagacgltbgcagtttacttactgaacgcaacttataactt	360
Db	307	ATCACACAGTGTCAAGGACAGAAAGCACTGCGCTGTATTACTGCACAGACTATATACTTG	366
QY	361	tacagcttcgagcaagggagcaacagltgtgaaataaaa	396
Db	367	TACACGTTTGGAGCTGGGACCAAGCTGGGAACGTGAAA	402

RESULT	13			
MUSIGKV130				
LOCUS	MUSIGKV130	339 bp	mRNA	29-OCT-1994
DEFINITION	Mus musculus Ig rearrange		ROD	
ACCESSION	L16819			
VERSION	L16819.1	GI:293622		
KEYWORDS	V-region; complementarity determining region; immunoglobulin light chain; kappa-immunoglobulin; processed gene.			
SOURCE	Mus musculus (strain NZB/W F1)		mRNA.	
ORGANISM	Mus musculus			
REFERENCE	Eukariyoti, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 339)			
TITLE	Justgaten,D.L., Kavalier,J., Gerhard,W. and Schaff,M.D.			
JOURNAL	The response to a foreign antigen in the autoimmune NZB/W F1 murine strain			
FEATURES	Unpublished (1993)			
source	Location/Qualifiers			
	1..339			
	/organism="Mus musculus"			
	/strain="NZB/W F1"			
	/db_xref="taxon:10090"			
	/cell_line="BM5-130"			
	/cell_type="hybridoma"			
	1..285			
V_region	/gene="Igk-V19"			
	1..324			
	/standard_name="V19"			
gene	/gene="Igk-V19"			
	70..102			
	/gene="Igk-V19"			
	/standard_name="CDRI"			
misc_feature	148..168			

	/gene="Iqk-V19"	/standard_name="CDR2"		
	265..291			
misc_feature	/gene="Iqk-V19"			
	/standard_name="CDR3"			
J_segment	286..324			
	/gene="Iqk-V19"			
	/standard_name="J1"			
BASE COUNT	89 a 85 c	88 g	76 t	1 others
ORIGIN				

Query Match	Similarity	74.5%:	Score 295:	DB 13:	Length 339:
Best Local	Similarity	92.3%:	Pred. No. 1.7e-91:		
Matches 310:	Conservative	0:	Mismatches 26:	Indels	Gaps
Qy	61	gacattgctgcgacacacatctccagattcccttgctcgtgaagcttagagaaagggccact	120		
Db	1	GACATTGGATGTGACNACTCTCCATCTCCCTCGCTGTCTCAGCAGGAGAAAGGTTACT	60		
Qy	121	attagctgcaaatccagtcacagtcacagtcctgcataacagtagaacccgagaaacttggct	180		
Db	61	ATGAGCTGCAATCCAGTCAGACAGTCTGCTCAACAGTAGAACCCGAGGAACTACTTGCT	120		
Qy	181	tgtgtaccgagaaacccgagcgacgtctctaactcgtcatctacttggcactcaactgg	240		
Db	121	TGTGTACCAGCAAGAAACCGAGGCGATCTCTTAACCTGCTGATCTACTGGGCACTCCACTAGG	180		
Qy	241	gaatctggagtcacctgcatcgcgtctcaagtgtgcagctgagatcttggaaacagattcaactcacc	300		
Db	181	GAACTGGGGGTCCCGATCGCTTCCACAGGCACTGGATGTGGGACAGATTTCACCTCACCC	240		
Qy	301	atcagcagctctgcagagctgaagaacgttgcagttattacatcgcacgcgaactctataactc	360		
Db	241	ATCAGCACTGTGCAGAGGCTGGAAGACCTGGCACTTTTATTACTGCAAGCAATCTTATATCT	300		
Qy	361	tacacgttcggacagagggagaccgaagttgaaataaa	396		
Db	301	TACACGTTTCGGAGGGGAGCAACGCTGGAATAATAAA	336		

RESULT 14	MDIGSVAI						
LOCUS	MDIGSVAI	336 bp	mRNA	ROD	05-NOV-1994		
DEFINITION	M.domesticus IgG variable region.						
ACCESSION	Z22039						
KEYWORDS	Z22039.1 GI:297576						
SOURCE	anti-DNA antibody; IgG gene; IgG variable region; immunoglobulin.						
ORGANISM	western European house mouse.						
	Mus musculus domesticus						
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;						
	Rodentia; Scurionath; Muridae; Murinae; Mus.						
REFERENCE	1 (bases 1 to 336)						
AUTHORS	Tilman,D.M., Jcu,N.T., Hill,R.J. and Marlon,T.N.						
TITLE	Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice						
	J. Exp. Med. 176 (3), 761-779 (1992)						
JOURNAL	9238144						
MEDLINE	2 (bases 1 to 336)						
REFERENCE	Marlon,T.N.						
AUTHORS	Direct Submission						
TITLE	Submitted (23-MAR-1993) Tony N. Marlon, Microbiology and Immunology, University of Tennessee, Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA						
JOURNAL	location/Qualifiers						
	1. 1336						
FEATURES	/organism="Mus musculus domesticus"						
source	/strain="(NZB x NZW)F1"						
	/isolate="mouse #163"						
	/db_xref="taxon:10092"						
	/chromosome="6"						
	/sex="Female"						
	/dev_stage="somatic variant"						

gene
CDS
/issue_type="spleen"
/cell_type="hybridoma"
/cell_line="163.1"
1..336
/gene="Igf"
<1..>336
/gene="Igf"
/function="Kappa light chain variable region for anti-DNA
antibody: VK8 family"
/note="163.1 is clonally related to the IgG hybridomas
163.14, 163.37, 163.64, 163.77, 163.106, 163.124, 163.132,
and 163.133 in the 163-cl clone"
/codon_start=1
/product="immunoglobulin variable region"
/protein_id="CA80013.1"
/db_xref="GI:297577"
/translation="DIVMSGPSLSVAGSEKVTMSCKSQSLNSTRKNTLAWYQ
KPGQSPKLIYMASTRSEGVDPDRFTSGSGTDTLTLLISSVQAEADLAVYCKOSYNLYT
FGGTRKLEIK"

BASE COUNT 90 a 82 c 88 g 76 t
ORIGIN

Query Match 73.9%; Score 292.8; DB 12; Length 336;
Best Local Similarity 92.0%; Pred. No. 9.8e-91;
Matches 309; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 61 gacattgtctgacacagcttcacagattccctgctgaagcttagagagagggccact 120
DB 1 GACATTGTGATGTCACAGCTCCATCCCTGGCTGTGCAGCAGAGAGAAAGTCACT 60
QY 121 attagctgcaatccagctcagagctgtctcaacagtagaacccgagagaaactattgct 180
DB 61 ATGAGCTGCAAAATCCACTCAGAGCTGCTCAACAGTAGAACCCGAAGAAGTACTTGCT 120
QY 181 tggtaaccagagaacacagggcgacctctaaactgtctactctactgtggcaaccag 240
DB 121 TGGTACACAGAGAAACAGGCGAGTCTCTAAACTGCTGATCTCTGGCATCCAGTAGG 180
QY 241 gaactcgtgggtccctgctcagcttcagctgagcagtgatctggagacagattcaactcacc 300
DB 181 GAATCTGGGGTCCCTGATCCCTTCACAGGCAAGTAGATCTGGACAGATTTCACCTCACC 240
QY 301 atcagcagcttcagagcttgaagcagctgtgcaattattacgcagcgaacttataactc 360
DB 241 ATCAGCAGTGTGAGGCTGAAGACTTGCAATTAATTAATTAATTAATTAATTAAT 300
QY 361 tacacgttcgacagggagacaaagtgaataaaa 396
DB 301 TACACGTTGGGGGGGGGACCAAGCTGGAATAAAA 336

RESULT 15
LOCUS MDIGKVAU 336 bp mRNA ROD 05-NOV-1994
DEFINITION M.domesticus Igk variable region.
ACCESSION Z22070
VERSION 222070.1 GI:297635
KEYWORDS anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.
SOURCE western European house mouse.
ORGANISM Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Tillingham,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.
TITLE Both IgM and anti-DNA antibodies are the products of clonally
JOURNAL selective B cell stimulation in (NZB x NZW)F1 mice
MEDLINE J. Exp. Med. 176 (3), 761-779 (1992)
92381444
REFERENCE 2 (bases 1 to 336)
AUTHORS Marion,T.N.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-1993) Tony N. Marion, Microbiology and

Immunology, University of, Tennessee, Memphis, 858 Madison Avenue,
Memphis, TN, 38163, USA
FEATURES
source location/Qualifiers
1..336
/organism="Mus musculus domesticus"
/strain="(NZB x NZW)F1"
/isolate="mouse #165"
/db_xref="taxon:10092"
/chromosome="6"
/sex="Female"
/dev_stage="somatic variant"
/tissue_type="spleen"
/cell_line="hybridoma"
/cell_line="165.5"
1..336
/gene="Igf"
<1..>336
/gene="Igf"
/function="Kappa light chain variable region for anti-DNA
antibody: VK8 family"
/codon_start=1
/product="immunoglobulin variable region"
/protein_id="CA80044.1"
/db_xref="GI:297636"
/translation="DIVMSGPSLSVAGSEKVTMSCKSQSLNSTRKNTLAWYQ
KPGQSPKLIYMASTRSEGVDPDRFTSGSGTDTLTLLISSVQAEADLAVYCKOSYNLYT
FGGTRKLEIK"

BASE COUNT 91 a 83 c 86 g 76 t
ORIGIN

Query Match 73.9%; Score 292.8; DB 12; Length 336;
Best Local Similarity 92.0%; Pred. No. 9.8e-91;
Matches 309; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 61 gacattgtctgacacagcttcacagattccctgctgaagcttagagagagggccact 120
DB 1 GACATTGTGATGTCACAGCTCCATCCCTGGCTGTGCAGCAGAGAGAAAGTCACT 60
QY 121 attagctgcaatccagctcagagctgtctcaacagtagaacccgagagaaactattgct 180
DB 61 ATGAGCTGCAAAATCCACTCAGAGCTGCTCAACAGTAGAACCCGAAGAAGTACTTGCT 120
QY 181 tggtaaccagagaacacagggcgacctctaaactgtctactctactgtggcaaccag 240
DB 121 TGGTACACAGAGAAACAGGCGAGTCTCTAAACTGCTGATCTCTGGCATCCAGTAGG 180
QY 241 gaactcgtgggtccctgctcagcttcagctgagcagtgatctggagacagattcaactcacc 300
DB 181 GAATCTGGGGTCCCTGATCCCTTCACAGGCAAGTAGATCTGGACAGATTTCACCTCACC 240
QY 301 atcagcagcttcagagcttgaagcagctgtgcaattattacgcagcgaacttataactc 360
DB 241 ATCAGCAGTGTGAGGCTGAAGACTTGCAATTAATTAATTAATTAATTAATTAAT 300
QY 361 tacacgttcgacagggagacaaagtgaataaaa 396
DB 301 TACACGTTGGGGGGGGGACCAAGCTGGAATAAAA 336

Search completed: August 27, 2000, 06:23:02
Job time: 2484 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 06:08:49 ; Search time 864.98 Seconds
(without alignments)
2018.881 Million cell updates/sec

Title: US-09-249-011-7
Perfect score: 396
Sequence: 1 atgattcacagggccaggtf.....ggaccacagtggaataaaaa 396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*

44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_est45:*
80: gb_est46:*
81: gb_est47:*
82: em_est35:*
83: em_est36:*
84: em_est37:*
85: gb_est48:*
86: gb_est49:*
87: gb_est50:*
88: gb_est51:*
89: gb_est52:*
90: gb_est53:*
91: gb_est54:*
92: gb_est55:*
93: gb_gss1:*
94: gb_gss2:*
95: gb_gss3:*
96: gb_gss4:*
97: em_gss1:*
98: em_gss2:*
99: em_gss3:*
100: em_gss4:*
101: gb_gss5:*
102: gb_gss6:*
103: gb_gss7:*
104: gb_gss8:*
105: gb_gss9:*
106: em_gss5:*
107: em_gss6:*
108: em_gss7:*
109: em_gss8:*
110: em_gss9:*
111: em_gss10:*
112: em_gss11:*
113: gb_gss10:*
114: gb_gss11:*
115: em_gss12:*
116: gb_gss12:*

Db	130	AAGTCAGGACGAGGTTTATTATACAGCTCCACCAATTAAGAACTCCTTAATTGTACAG	189
Qy	190	cagaataccaagagcagacctcttaactgctgcgactactactgggactccaactggaaactgg	249
Db	130	CTGAATACCAAGGACACCTCTCTTAAGATGATCATTTACTGTGGCATCTACCCGGGAATCCGGG	249
Qy	250	gtccctgatcgttcagtgagtgatctgggagacagattcaacttcacatacgaagcagt	309
Db	250	GTCCCTGACCAATTCAGTGTGGCAGCCGGGTCTGGGACAGATTTTACCTCTACCATCAGCGGC	309
Qy	310	ctgcagcgtgaagacgttgcagtttacttactgcagcgaactcttaatactt--tacacg	366
Db	310	CTGCAGGCTGAAGATGTGGCACTTATTACTGTACAGCAATATCATAGTATTCGGTACACT	369
Qy	367	ttcgagcagggagccaaggtggaataaaa	396
Db	370	TTTGCCAGGGGACCAAGCTGGAGATCAAA	399
RESULT	4		
LOCUS	AM404610	550 bp mRNA	EST 16-FEB-2000
DEFINITION	UI-HF-BL0-acc-a-06-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone		
ACCESSION	IMAGE:3058451 5', mRNA sequence.		
VERSION	AM404610		
KEYWORDS	AM404610.1 GI:6923667		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia: Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 550)		
COMMENT	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/imap/image.html Seq primer: M13 Forward.		
FEATURES	Location/Qualifiers		
SOURCE	1..550		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:3058451"		
	/clone_1lb="NIH_MGC_37"		
	/tissue_type="lymph"		
	/cell_type="germinal center B cells"		
	/cell_line="MGC85"		
	/lab_host="DH10B (LTI)"		
	/note="Vector: pUT3-Pac; Site_1: NotI; Site_2: Eco RI; constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
BASE COUNT	140 a 150 c 139 g 121 t		
ORIGIN			
Query Match	57.2%	Score 226.6	DB 72; Length 550;
Best Local Similarity	79.6%	Pred. No. 2.4e-59;	
Matches	281; Conservative	0; Mismatches 69;	Indels 3; Gaps 1;
Qy	47	ctgagcactgtggtgaacctgtgtgcgaacaatccagattccctggtgtaagctgag	106
Db	8	CTGTGCGCTTACGGGACATCGATGATGACCACTCTCCAACTCCCTGGGTGTCTCTGG	67

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Matches 279; Conservative	79.58;	224.6;	DB 72;	630;	0;	69;	3;

Oy 49 ggaacitgtggggaattgtctgtcaaacagctccagaatccctgctgtgaagttaga 108
 Db 8 ggtgccttagcggggaatgctatgatacccaagctccagatccctggctgtcttccggc 67
 Oy 109 gagaagggacatatagctgcaaatccagatcagaagctcgtccaaacagtagaacccgag 168
 Db 68 gagagggccaccatcattcaactgcagaagtcacagagcttTTATACACTCCACAAATAAG 127
 Oy 169 aactactgtgcttgtgtaccagcagaacaacagcagcctccaaactcgtcatctatg 228
 Db 128 AATTCTTAGATTGGTACACAGAAACAGACAGAGCTCTTAAGTCGTCATTTCTGG 187
 Oy 229 gcatccactaaggaaactcgtgggtccctgtatcgtcttcagtgcaatgtgacatcgtggacagat 288
 Db 188 GCATTTACCCGGGGAATCCGGGGTCCCTCAGATTTCAGATGCGACAGGGGTCTGGGACAGAT 247
 Oy 289 ttcaactccaccatcagaagctcgtcgaagctgaagaagctgtgaattattactgaagcaa 348
 Db 248 TTCACCTTCACCAATCAGACAGCCTSCAAGCCTGAATGCGAGTTTATCTGTGCACAA 307
 Oy 349 tctataatctct---tacacgttgggaagggagcacaagtggaataaataa 396
 Db 308 TATTATAGTATTTCCCTTCACCTTGGCCCAAGGACAGACTGGAGATTAA 358

[illegible]

ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi, Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 328)
AUTHORS	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
TITLE	National Institutes of Health, Mammalian
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: robert.strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/TLNU at: www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES

SOURCE

BASE COUNT
ORIGIN

Query Match	Similarity	55.8%	Score 220.8	DB 72	Length 328
Best Local	Similarity	81.7%	Pred. No. 1.3e-57		
Matches 255	Conservative	0	Mismatches 57	Indels 0	Gaps 0
QY	53	cctgtgaggacattgctgcacacagctctccagatccctgtgctgtaagcttagagaga	112		
Db	8	cctagggggacatcgatgatgacccacagctccagactccctggctgctcgtggcgagag	67		
QY	113	ggggccactattgctgcgaataaccagtcagtgctcgtctcaacagtagaaccggaanaact	172		
Db	68	ggggccaccattcaacgcgaagtcacagcaagtggtttatcacagctccacaatataagact	127		
QY	173	acttgctgtgtgacacagcaaacagggcgacctctctaactgtcgtactactgtggact	232		
Db	128	acttgacttgtaacacgcaaaacaggaagctctctaaagctcatttatctggggcatt	187		
QY	233	ccactaggaatctggggtccctgatacgcttaagtcagtcagtcagatcttggaacagattca	292		
Db	188	ctaacccgggaattccgggggtccctgaaccatttcagttggcagcggggtttgggacagatttca	247		
QY	293	ctctcaccaatcagcagctctgcaggtgaagacgtlbgcagttattacttcaacgaacactt	352		
Db	248	ctcttcacacattcagcagccctcgacggctgaagatgtgcacatttatctcagcacaattatt	307		
QY	353	ataactcttaca	364		
Db	308	atagtaactctca	319		

RESULT	7		
AA300651			
LOCUS	AA300651	363 bp	mRNA
DEFINITION	EST13764 Testis tumor Homo sapiens CDNA 5' end similar to similar	EST	18-APR-1997
	to immunoglobulin light chain, V region, anti-lipid A, mRNA		
	sequence.		
ACCESSION	AA300651		
VERSION	AA300651.1	GI:1953221	
KEYWORDS	Est.		
SOURCE	human.		

ORGANISM	REFERENCE	AUTHORS
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
1 (bases 1 to 363)		
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,		

TITLE	Initial assessment of human gene diversity and expression patterns
JOURNAL	based upon 83 million nucleotides of CDNA sequence
MEDLINE	Nature 377 (6547 Suppl.), 3-174 (1995)
COMMENT	12140200
	Other_ESTs: THC102133

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel.: 3018699056
Fax: 3018699423
Email: arkerlavet@igr.org
For clone availability, additional sequence and ex

JOURNAL Unpublished (1999)
On May 7, 1998 this sequence version replaced gi:3119232.
COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the RAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM4<2=PM4-HT0348-261199-001-B11<3=1999-11-26<4=1)

Seq primer: puc 18 forward

High quality sequence start: 10

High quality sequence stop: 441.

Location/Qualifiers

1. 459

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HT0348"

/dev_stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 110 a 123 c 118 g 107 t 1 others

ORIGIN

Query Match 50.5%; Score 200; DB 71; Length 459;

Best Local Similarity 79.8%; Pred. No. 3.5e-51;

Matches 249; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 88 tccctgctgtagcttgagagaggggcccattatagctgaatccagtgtaagctcg 147

Db 16 tccctgctgtagcttgagagaggggcccattatagctgaatccagtgtaagctcg 75

QY 148 ctcaacatgagaccgagaggaactactgctgtgtacacagagaacagagcgagct 207

Db 76 ttgtacagctccacacatgaggaactactgctgtgtacacagagaacagagcgagct 135

QY 208 cctaactgctgtagcttgagagaggggcccattatagctgaatccagtgtaagctcg 267

Db 136 cctaactgctgtagcttgagagaggggcccattatagctgaatccagtgtaagctcg 195

QY 268 ggcagtgtagcttgagagaggggcccattatagctgaatccagtgtaagctcg 327

Db 196 ggcagtgtagcttgagagaggggcccattatagctgaatccagtgtaagctcg 255

QY 328 ggcagtgtagcttgagagaggggcccattatagctgaatccagtgtaagctcg 384

Db 256 ggcagtgtagcttgagagaggggcccattatagctgaatccagtgtaagctcg 315

QY 385 gtggaataaaa 396

Db 316 gtggaataaaa 327

RESULT 10

AM407858 323 bp mRNA EST 16-FEB-2000

LOCUS UI-HF-BL0-adi-c-05-0-UI-r2 NIH_MGC_37 Homo sapiens cDNA clone

DEFINITION IMAGE:3061617 5', mRNA sequence.

ACCESSION AM407858

VERSION AM407858.1 GI:6926915

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 323)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jan 6, 2000 this sequence version replaced gi:6676906.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CNA Library Preparation: M.B. Soares Lab

CNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnl.gov/dbp/image/image.html

Seq primer: M13 Forward.

Location/Qualifiers

1. 323

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:3061617"

/clone_lib="NIH_MGC_37"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTR)"

/note="Vector: pRT3-Pac; Site_1: NotI; Site_2: Eco RI; constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaudo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 75 a 92 c 76 g 80 t

ORIGIN

Query Match 49.0%; Score 194.2; DB 72; Length 323;

Best Local Similarity 82.3%; Pred. No. 2e-49;

Matches 223; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 67 gtgcagacagcttcacacatccctgctgtaagcttgagagagggccactatgac 126

Db 9 gtgcagacagcttcacacatccctgctgtaagcttgagagagggccactatgac 68

QY 127 tgcacatccagtcagagctgctcaacagtagaacccgagaggaactactgctgtgac 186

Db 69 tgcacatccagtcagagctgctcaacagtagaacccgagaggaactactgctgtgac 128

QY 187 cagcagaacccagcagcctcctaaactgctgactactgagcagcagcagcagcagc 246

Db 129 cagcagaacccagcagcctcctaaactgctgactactgagcagcagcagcagcagc 188

QY 247 ggggtccctgagctgctgagctgagctgagctgagctgagctgagctgagctg 306

Db 189 ggggtccctgagctgctgagctgagctgagctgagctgagctgagctgagctg 248

QY 307 agctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 337

Db 249 agctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 279

RESULT 11

AI734035 425 bp mRNA EST 14-JUN-1999

LOCUS AI734035

DEFINITION IMAGE:741867 5' similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II

ACCESSION AI734035

VERSION AI734035.1 GI:5055148

KEYWORDS EST.

SOURCE human.

Db 210 AAGCAGGAGGAGTCTCCACAGCTCTGATCTATTGGGTTTAAACGGGCTCCGGGGTTC 269
Oy 253 cctgctgcttcagtgagtgatctggtgagacatttaccctaccatcgacgtctg 312
Db 270 CCTGACAGGTTGAGTGGCAGTGTGATCAGCAGACATTATTAACAAAATTCAGAGAGTG 329
Oy 313 caggtcgaagacgtgagcttattacttcacgcaatct---tataatcttcacgcttc 369
Db 330 GAGCGTGAAGAGTGTGGGTTTATCAGTCATGCAGCGCTCTCAATCTCTCAGACTTTT 389
Oy 370 ggaacgggagaccaggtggaataaaa 396
Db 390 GGCCAGGGAGCCAGCTGGAGATCAAA 416

RESULT 13
AM406796 423 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BL0-acz-f-08-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3060998 5', mRNA sequence.
ACCESSION AM406796
VERSION AM406796.1 GI:6925853
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jan 6, 2000 this sequence version replaced gi:6675816.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward
Location/Qualifiers
1. 423
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3060998"
/clone_1id="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTR)"
/note="Vector: pTR73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonardo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 98 a 125 c 108 g 92 t
ORIGIN

Query Match 47.6%; Score 188.4; DB 72; Length 423;
Best Local Similarity 69.9%; Pred. No. 1.3e-47;
Matches 277; Conservative 0; Mismatches 101; Indels 18; Gaps 1;

Oy 1 atgagttcacagccaggttcttatatgctgctgctatggtatgacacgtgag 60
Db 14 ATGAGAGCCCGCCAGCTCTCTCCCTCCGCTACCTACCTCCACATACCACTGGA 73
Oy 61 gacattgtctgacacagctccagattccctgctgtaagttagagagggccact 120

Db 74 GAATAGTAGATGACGACAGCTCCACAGCCACCCTGTCTGTCTCCAGGGGAAAGACCCACC 133
Oy 121 attagctgaatccagtcagagtcgtctcaacagtagaaccggagaaactactgct 180
Db 134 CTCTCTCCAGGGCCAGTCAGAGTGTGTAGCA-----ACTTAGCC 175
Oy 181 tggtaaccgagaaacccagggagcctcctaactcgtcgtactactggtgacaccagtg 240
Db 176 TGGTACCAACAGAAACCTGGCCGGGCTCCAGGCTCTCACTATGATGATCCACCGAG 235
Oy 241 gaatcgggtccctcgtatcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
Db 236 GCCACTGATATCCAGTAGAGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 295
Oy 301 atcagcagctcgcaggtcgaagcgtgagcttattacttcagcagcaactataactt 360
Db 296 ATCAGCAGCTGCACTGCAAGATCTTCTAGTATCTGACAGCACTATGATGATGATGATG 355
Oy 361 tacacgttcgacagggagcagaggtggaataaaa 396
Db 356 CAAAGCTTGCCAGAGGACCAAGGTGGAATCAAA 391

RESULT 14
AM405725 488 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BL0-abv-f-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3057944 5', mRNA sequence.
ACCESSION AM405725
VERSION AM405725.1 GI:6924782
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 488)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward
Location/Qualifiers
1. 488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3057944"
/clone_1id="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTR)"
/note="Vector: pTR73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonardo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 105 a 129 c 129 g 125 t
ORIGIN

Query Match 46.0%; Score 182.2; DB 72; Length 488;
Best Local Similarity 72.0%; Pred. No. 1.1e-45;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 06:25:32 ; Search time 72.06 Seconds

(without alignments)
1374.911 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396

Sequence: 1 atgattcaacagccagctg.....ggacacagtggaataaaa 396

Scoring table: IDENTITY_NNC

Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	340	85.9	480	1	N91663	Light chain of mon
2	332	83.8	952	1	O94036	Mab 55.1 light cha
3	301.4	76.1	439	1	T60729	CDNA encoding huma
4	301.4	76.1	439	1	T60730	CDNA encoding huma
5	298.2	75.3	399	1	O66845	Sequence encoding
6	293.6	74.1	402	1	T43415	Xenograft antibody
7	288.6	72.9	399	1	Q74067	Monoclonal antibody
8	288.6	72.9	439	1	T60734	CDNA encoding wild
9	286.8	72.4	418	1	T34152	Monoclonal antibody
10	285.4	72.1	439	1	T72268	Monoclonal antibody
11	285.4	72.1	460	1	T72238	Chimeric Mab 15 PC
12	283.2	71.5	342	1	X34465	Mouse Mab 6A4 light
13	279.8	70.7	1443	1	O62958	Glycophorin antibo
14	277.8	70.2	747	1	V36237	DNA od ScFv D3M wh
15	275.8	69.6	870	1	O62956	Glycophorin antibo
16	275.2	69.5	660	1	O53430	Sequence encoding
17	270.6	68.3	330	1	V29839	Fusion protein p1c
18	270.6	68.3	864	1	V72072	Fusion protein p1c
19	270.6	68.3	2019	1	V72059	Fusion protein p1c
20	270.6	68.3	2025	1	V72064	Fusion protein p1c
21	267.2	67.5	336	1	X34588	Mouse Mab 6A4 muta
22	267.2	67.5	1701	1	O30919	Anti-DNA IL/TM (H2
23	267.2	67.5	1701	1	O30920	Anti-DNA IL/TM (H2
24	261.4	66.0	400	1	N80499	Vector pMDR1007. N
25	260.8	65.9	511	1	N80499	Encodes v region o
26	257.4	65.0	398	1	O66699	EST clone AY241. N
27	257.4	65.0	798	1	O34842	DRG-200 Ab light
28	250.2	63.2	407	1	O26047	Encodes V kappa reg
29	248.6	62.7	402	1	T00780	V-region of L-chain
30	248.6	62.7	344	1	O30900	E-selectin-specific
31	247	62.4	5703	1	T34110	Insert pMDR1003. N
32	247	62.4	5703	1	V03504	Anti-IL-5 humanise
33	241.6	61.0	336	1	O30881	Plasmid pCNI15H2LC
						5A8 VL. New anti-C

34	241	60.9	340	1	O30880	pMDR927 insert. Ne
35	239.8	60.6	340	1	O73232	Murine L chain fro
36	238.6	60.3	795	1	O04263	Encodes Colon Canc
37	238.2	60.2	342	1	O23341	Murine kappa chain
38	238.2	60.2	342	1	O74303	Mouse Hmrl light
39	237.8	60.1	1373	1	N80941	Encodes Vchi regio
40	236.6	59.7	339	1	O68710	Humanised Mab L-ch
41	236.6	59.7	340	1	O32776	Light chain variab
42	236.2	59.6	619	1	N80498	Encodes v region o
43	233.6	59.0	1479	1	X34596	DNA encoding a com
44	233.4	58.9	339	1	O44841	Mab NPS2 light cha
45	233.4	58.9	726	1	T18829	Single chain murin

ALIGNMENTS

RESULT 1	
ID N91663	N91663 standard; DNA: 480 BP.
AC N91663:	
DI 14-MAR-1990 (first entry)	
DE Light chain of monoclonal antibody 6A4.	
KW Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.	
FH Key	Location/Qualifiers
FT cds	37..480
FT	/*tag= a
FN	EP-338395-A.
PD	25-OCT-1989.
PF	12-APR-1989; 106463.
PR	19-APR-1988; DE-813023.
PA	(BEHM) Behringwerke.
PI	Domdey H, Marger M, von Specht BU.
DR	WPT-89-310861/43.
DR	P-PSDB: P93078.
PT	Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
PS	variable antibody regions.
PS	Claim 1; page 6; 7pp; german.
CC	The sequence has a variable and constant region. Monoclonal antibody 6A4
CC	reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa.
CC	It is used for therapy and diagnosis of infection, and as a carrier for
CC	drugs. The antibody is IgG2a subclass.
SQ	Sequence 480 BP; 115 A; 118 C; 135 G; 112 T;

Query Match 85.9%; Score 340; DB 1; Length 480;
Best Local Similarity 91.2%; Pred. No. 1.4e-102;
Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1	atgattcaacagccagcttctattatgtcgtcgtcatggtatcggccctgtgg 60		
DB 37	ATGGATTCAACAGCCAGCTTCTTATTATGCTGCTATGGGTCTGGTGGG 96		
QY 61	gacattgtctacacagctcaccagattccctgtcgttaagttagagagagccact 120		
DB 97	GACATTGTCTACACAGCTCCTCCTCCCTGCTGTGTTCAGCAGAGAGACTACT 156		
QY 121	attagctgcaaatcagctcagctcgtcctcaacagtagaaccggagagaacttggct 180		
DB 157	ATGACTGCAAAATCCAGTCAAGTCTGCTCAACAGTATACCCGAAGAACTTCTGGCT 216		
QY 181	tgttcacagcagaacacccagggagagctcctcaactgcgtcgtattatggcaccactgg 240		
DB 217	TGTTACCAAGCAAAACCAAGGCGAGTCTCTTAACGCTGATTTACTGGCACTACAG 276		
QY 241	gacattgagctccctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 300		
DB 277	GATCTGGGCTCCCTGATCGCTTTCACAGCAGTGGATCTGGAGATTTCTCTCACC 336		
QY 301	atcagcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 360		
DB 337	ATCAGCAGTGTCAAGCAGTGAAGACCTGGCAGTTTATCTCAACCAATCTTATATCTT 396		

OY 361 tacacgttcgacaggggaccacgaagtggaaataaa 396
|||||
Db 357 CGGACGCTTCGGTGGAGGACACCAAGCTGGAAATCAAA 432

RESULT 2

O94036 standard; cDNA: 952 BP.
ID O94036:
AC 21-NOV-1995 (first entry)
DE Mab 55.1 light chain cDNA.
KW Antigen binding structure; complementarity determining region; CDR;
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin; ss.
OS Mus sp.
FH Key
FH cds Location/Qualifiers
FT signal_peptide 16..75 /*tag= a
FT mat_peptide 76..732 /*tag= b
FT /*tag= c
PN WO9515382-A.
PD 08-JUN-1995.
PE 29-NOV-1994: G02610.
PR 03-DEC-1993: GB-024819.
PR 03-JUN-1994: GB-011089.
PA (ZENE) ZENECA LTD.
PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
PI Rose MS, Wright AF;
PI WPI: 95-215262/28;
DR P-PSDB: R76087.
DR Antigen binding structures containing CDRs recognising the CA55.1
PT antigen - produced by hybridomas and host cells, for use in the
PS diagnosis and therapy of cancer
PS Disclosure: Fig.16; 121pp: English.
CC Mab 55.1 (BCACC 93081901) recognises the colorectal tumor-associated
CC antigen CA55.1. cDNAs for the heavy (O94037) and light (O94036)
CC chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or
CC V-mu humanized 55.1 constructs have been expressed in myeloma
CC cells and E. coli.
SQ Sequence 952 BP: 245 A; 268 C; 215 G; 224 T;

Query Match

Best Local Similarity 83.8%; Score 332; DB 1; Length 952;
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 1 atgattcacagggccaggtctctattatgtctgtctgtatgggtatctggcactgtgg 60
|||||
Db 16 ATGATGATTCACAGGCCACAGTCTTATATTCCTGCTGTAAGGTAATCTGGAACTGTGG 75
61 gacattgtctgcacacagttccagattccctgtctgttaagcttagagagagggccact 120
|||||
Db 76 GACATTGTGATGTCACAGTCTCCATCCTCCCTGGCTGTGTGCACAGAGAGAAAGGTCAC 135
121 attagctgcaaatccacgtcagaatctgtctcaacaagttagaaccggagagaactcttgct 180
|||||
Db 136 ATGAGTGTGCAAAATCCAGATCCAGATCTCTTCMACAGTAAGAACCCGAAGAATCTTGGCT 195
181 tggttaccagagaagaaccagggcagctctcctaactctgaattacatcagggatccacttag 240
|||||
Db 196 TGGTACACAGAGAGACAGGCGAGTCTCTTAACCTGCTGATCTATTGGGCAATCCACTAGG 255
241 gaattcgtgggtccctcgtatcgtctcagtgagtgagtgagttctggacagaattcactcacc 300
|||||
Db 256 ACATCTGGGGTCCCTGATGCTTACACAGGAGTGGATCTGGGACAGATTTCACATCTCAC 315
301 atcagcagctcgcaggtcgaagacgttgcagttattactgaagcaatcttataactc 360
|||||
Db 316 ATCAGCAGTGTGACAGCTGTAAGACTGTGGCAATTATTACTGCAAGCAATCTTACTCTT 375

OY 361 tacacgttcgacaggggaccacgaagtggaaataaa 396
|||||
Db 376 CGGACGCTTCGGTGGAGGACACCAAGCTGGAAATCAAA 411

RESULT 3

T60729 standard; cDNA: 439 BP.
ID T60729:
AC T60729:
DE 25-SEP-1997 (first entry)
KW cDNA encoding humanised murine anti-E-selectin antibody CY1788V(LA).
KW Humanised; murine; mouse; E-selectin; antibody; light chain;
KW variable region; detection; inhibition; mediation; cell adhesion;
KW diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
KW acute respiratory distress syndrome; gross cystic breast disease;
KW cancer; treatment; splanchic occlusion shock; psoriasis;
KW complement; chimeric; ds.
OS Chimeric - Mus spp.
OS Chimeric - Homo sapiens.
OS Synthetic.
FH Key
FH cds Location/Qualifiers
FT signal_peptide 16..426 /*tag= a
FT /*tag= "no stop codon given"
PN MO9640942-A1.
PD 19-DEC-1996.
PE 06-JUN-1996: U09204.
PR 07-JUN-1995: US-482112.
PA (CYTE-) CYTEL CORP.
PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;
PI Jones S;
PI WPI: 97-077272/07.
DR P-PSDB: W10544.
DR Humanised anti-E-selectin antibody - useful for diagnosis and
PT treatment of, e.g. inflammatory responses, septic shock, acute
PT respiratory distress syndrome or cancer
PS Claim 29: Page 69; 189pp: English.
CC The present sequence encodes the humanised murine anti-E-selectin
CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can
CC be used to detect E-selectin, or inhibit E-selectin mediated cell
CC adhesion. It can also be used to diagnose, reduce or inhibit an
CC inflammatory response, or the severity of pathologies, e.g. septic
CC shock, acute respiratory distress syndrome, wound associated
CC sepsis, gross cystic breast disease or cancer, or treat, e.g.
CC splanchic occlusion shock, or psoriasis. It can be administered to
CC a human without inducing an immune response. In addition, the
CC effector portion of the Ab can interact with various components of
CC the human immune system, including complement.
SQ Sequence 439 BP: 106 A; 110 C; 117 G; 106 T;

Query Match

Best Local Similarity 76.1%; Score 301.4; DB 1; Length 439;
Matches 345; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

OY 1 atgattcacagggccaggtctctattatgtctgtctgtatgggtatctggcactgtgg 60
|||||
Db 28 ATGAGTGTGCAAAATCCAGATCCAGATCTCTTCMACAGTAAGAACCCGAAGAATCTTGG 87
61 gacattgtctgcacacagttccagattccctgtctgttaagcttagagagagggccact 120
|||||
Db 88 GACATTGTGATGTCACAGTCTCCATCCTCCCTGGCTGTGTGTGCGGACAGAGGCCAC 147
121 attagctgcaaatccacgtcagaatctgtctcaacaagttagaaccggagagaactcttgct 180
|||||
Db 148 ATCAACTGCAAAATCCAGATCCAGATCTGTGTACACAGTGAAGAAATCAAGAACTTGAAC 207
181 tggttaccagagaagaaccagggcagctctcctaactctgaattacatcagggatccacttag 240
|||||
Db 208 TGGTACACAGAGAGACAGGCGAGTCTCTTAACCTGCTGATCTATTGGGCAATCCACTAGG 267
241 gaattcgtgggtccctcgtatcgtctcagtgagtgagttctggacagaattcactcacc 300

DB	GAATGTGGGGTCCCGATGCGTTCACTGAGTGCATGATCTCGAACAAGATTTCACCTCAC	327
OY	301 atcagcagctctgcaggtctgaagacgttgcagttattactgcagcaatcttata--at 357	
DB	338 ATCACCAGACTCTCAGAGCTGACAGACGTCGACAGTTTATTACTGTCAGAAATGATTAGTTAT	387
OY	358 cttaacagcttcgcagcaggggccaagtcggaataataa 396	
DB	388 CCGCTCACGCTTGGTCMAAGGACCAAGCTGGAGATTAAAA 426	
RESULT	4	
ID	T60730 standard; cDNA: 439 BP.	
AC	T60730:	
DT	25-SEP-1997 (first entry)	
DE	cDNA encoding humanised murine anti-E-selectin antibody CY1788V(LB).	
KW	Humanised; murine; mouse; E-selectin; antibody; light chain;	
KW	variable region; detection; inhibition; mediation; cell adhesion;	
KW	diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;	
KW	acute respiratory distress syndrome; gross cystic breast disease;	
KW	cancer; treatment; splanchic occlusion shock; psoriasis;	
KW	complement; chimeric; ds.	
OS	Chimeric - Mus spp.	
OS	Chimeric - Homo sapiens.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	cds	16..426
FT		/*tag= a
FT		/note= "no stop codon given"
FM		
FN	W09640942-A1.	
PD	19-DEC-1996.	
PF	06-JUN-1996; U09204.	
PR	07-JUN-1995; US-482112.	
PA	(CYTE-) CYTEL CORP.	
PI	Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;	
PI	Jones S;	
DR	WPI: 97-077272/07.	
DR	P-PSDB; W10545.	
PT	Humanised anti-E-selectin antibody - useful for diagnosis and	
PT	treatment of, e.g. inflammatory responses, septic shock, acute	
PT	respiratory distress syndrome or cancer	
PS	Claim 29; Page 71: 89pp; English.	
CC	The present sequence encodes the humanised murine anti-E-selectin	
CC	antibody (Ab) light chain variable region, CY1788V(LB). The Ab can	
CC	be used to detect E-selectin, or inhibit E-selectin mediated cell	
CC	adhesion. It can also be used to diagnose, reduce or inhibit an	
CC	inflammatory response, or the severity of pathologies, e.g. septic	
CC	shock, acute respiratory distress syndrome, wound associated	
CC	sepsis, gross cystic breast disease or cancer, or treat, e.g.	
CC	splanchnic occlusion shock, or psoriasis. It can be administered to	
CC	a human without inducing an immune response. In addition, the	
CC	effector portion of the Ab can interact with various components of	
CC	the human immune system, including complement.	
SC	Sequence 439 BP; 106 A; 110 C; 118 G; 105 T;	
Query Match	76.1%; Score 301.4; DB 1; Length 439;	
Best Local Similarity	86.5%; Pred. No. 7e-90;	
Matches 345; Conservative	0; Mismatches 51; Indels 3; Gaps	
OY	1 atgagctcacagcagccaggtctcttatatgcgcgcgtatcgtatcgtgcaccttggg 60	
DB	28 ATGAGCTCACACATTCCAGTCTCCTCATGTCCTCCCTGCTTTTGGGTATCTGTA	87
OY	61 gacatctgtctgcagacagctccagattcccttgccttgaagcttagagagagggccact 120	
DB	88 GACATCTGTATGATACACAGCTCCAGACTCCCTGGCTGTCTCTCTGCGGAGAGGGCACC 147	
OY	121 atagctggaataatccagctagagctctgcctcaacagagagaccggagagaaactcttgct 180	
DB	148 ATCACTCTGGAAGTCCAGTGAAGTCTGTTACACAGTGAAGTCAAAAGAACTACTTGACC 207	

Query Match	Best Local Similarity	Matches 343: Conservative	Score 298.2: DB 1: Length 399: Pred. No. 7.6e-89: Mismatches 53: Indels 3: Gaps 1:
181	tggtacacagcaaaaacacagggagccgctctctaaactgcgtgacttacttgggcatccacagg	240	240
Db	208	tggTTCACAGCAAAACACAGGCGACCTCTTAAGCTGTTGATCTTACTGGGCATCCACTAGG	267
Qy	241	gaatctgggggtccctcgatcgcgtcttcagttgagcagtgatctggagacagatttcactccacc	300
Db	268	GAATCTGGGGGTCCCGATCGGCTTCAGTGGAGTGGATGCTGGAAAGATTTCACCTCACC	327
Qy	301	atcagcagctcgcaggtcgaagcgtgagcagtttatctcgaagcaattctata--at 357	357
Db	328	ATCAGCAGCTCGCAGGCTGGAAGACCTGGCAGTTTATCTGTGCAGAAAGATTATAGTTAT	387
Qy	358	cttiacacgttcgcagcagggagacaaagttggaataaaa 396	396
Db	388	CCGCTCAGCTTCGTCAGAGGACCAAGGTGAGATATAAA 426	426
RESULT 5	066845		
ID	066845	standard; DNA; 399 BP.	
AC	Q66845		
DT	31-DEC-1994	(first entry)	
DE	Sequence encoding the light chain variable region of the mouse NA-8		
DE	antibody, including the signal sequence and mature chain.		
KW	Antibody NA-8; human CD18; complementarity determining region; CDR;		
OS	ss.		
FN	Mus musculus.		
FT	Key	Location/Qualifiers	
FT	cds	1..399	
FT		/*tag= a	
PN	MO9412214-A.		
PD	09-JUN-1994.		
PF	30-NOV-1993; U11611.		
PR	01-DEC-1992; U5-983949.		
PA	(PROT-) PROTEIN DESIGN LABS INC.		
PI	Co MS, Landolfi NF;		
DR	WPI: 94-199973/24.		
DR	P-RSDB: R59509.		
PT	New humanised antibodies specific for CD18 - derived from new		
PT	murine antibody NA-8, prevent binding of neutrophils to		
PT	endothelial cells, useful for treating inflammation		
PS	Disclosure: Fig 1A; 50pp; English.		
CC	The mouse antibody NA-8 binds to human CD18. cDNAs for the heavy		
CC	chain and light chain variable domain genes of NA-8 were cloned		
CC	using anchored PCR. The cDNA variable domain sequences and the		
CC	deduced AA sequences are shown in Q66845/R59509 and Q66846/R59510.		
CC	Sequence 399 BP; 102 A; 88 C; 100 G; 109 T;		

Query Match	Best Local Similarity	Matches 332: Conservative	74.1% 83.8%	Score 293.6: Pred. No. 2.5e-87;	DB 1:	Length 402:	0:
0Y 1 atggattccacagggccagagctctctattgtcgtcgtcatagtgtaatcggcacctctggg	1 atggattccacagggccagagctctctattgtcgtcgtcatagtgtaatcggcacctctggg	0: Mismatches 64; Indels 0; Gaps 0;					
Db 1 ATGGATATCACAGACACACAGAGTCTCTCATGTGCTCTGCTGCTCTGGGATCTGTGTAACCTGTGGG	1 ATGGATATCACAGACACACAGAGTCTCTCATGTGCTCTGCTGCTCTGGGATCTGTGTAACCTGTGGG						
0Y 61 gacattgtgctgacacagctctccagattccctgctgctgaaggttagagagagggccact	61 gacattgtgctgacacagctctccagattccctgctgctgaaggttagagagagggccact						
Db 61 GACATTGTGATGATGACCCAGACTCCACTCTCCAGGCTGTGTACAGCAGGGAGAGAGGTCACT	61 GACATTGTGATGATGACCCAGACTCCACTCTCCAGGCTGTGTACAGCAGGGAGAGAGGTCACT						
0Y 121 attagctgcaaatccagtcagatcagatctgtctcaacagtagaaccggagaactacttgct	121 attagctgcaaatccagtcagatcagatctgtctcaacagtagaaccggagaactacttgct						
Db 121 ATGAGACTCTCAAGTCCAGTCAGTCAGAGCTTTTATTAACAATGAAAAAATAAACAATCTTGCC	121 ATGAGACTCTCAAGTCCAGTCAGTCAGAGCTTTTATTAACAATGAAAAAATAAACAATCTTGCC						
0Y 181 tggtaaccagcagaacacccgggagcagctccctaaacgctgcatctactctggcatccactag	181 tggtaaccagcagaacacccgggagcagctccctaaacgctgcatctactctggcatccactag						
Db 181 TGGTACCGGCAAAACACAGGCGCAGTCTCTTAACGTCGATTACTGGGCACTCCACTAGG	181 TGGTACCGGCAAAACACAGGCGCAGTCTCTTAACGTCGATTACTGGGCACTCCACTAGG						
0Y 241 gaatctgggagtcctctgcatcgtctcagctgagctgagatcttgagacagatttcaactcacc	241 gaatctgggagtcctctgcatcgtctcagctgagctgagatcttgagacagatttcaactcacc						
Db 241 GAATCTGGGAGTCCCTCGATCGCTTCACTAAGGAGTGTGATCTGGGACAGATTTCCTACTGTGAC	241 GAATCTGGGAGTCCCTCGATCGCTTCACTAAGGAGTGTGATCTGGGACAGATTTCCTACTGTGAC						
0Y 301 atcagcatctctgcagagctcgaagacgttgacagatttactcagcagaactctataactt	301 atcagcatctctgcagagctcgaagacgttgacagatttactcagcagaactctataactt						
Db 301 ATCAGCATCTGTCACAGCAGAAAGACCTGGCTGTTTATTAATGTCACACAGTACTAATACTTG	301 ATCAGCATCTGTCACAGCAGAAAGACCTGGCTGTTTATTAATGTCACACAGTACTAATACTTG						
0Y 361 tacacgttcgagcagggagaccagagctggagaataaa	361 tacacgttcgagcagggagaccagagctggagaataaa						
Db 361 TACACGTTTGGAGCTGGGACCAAGCTGGAACTGAA	361 TACACGTTTGGAGCTGGGACCAAGCTGGAACTGAA						
RESULT 7							
074067	074067						
AC 074067:	074067 standard; DNA: 399 BP.						
DT 02-JUL-1996	(first entry)						
DE Monoclonal antibody; CB-Hep.1, light chain variable domain cDNA.							
KW HBV; hepatitis B virus surface antigen; monoclonal; antibody; Fv;							
KW CB-Hep.1; immunoprecipitation; detection; hybridoma; recombinant; Fv;							
KW variable; VH; HBSAg; ss.							
OS Mus sp.							
PH Key	Location/Qualifiers						
FT cds	1..399						
FT /+tag=	a						
FT signal_peptide	1..60						
FT /+tag=	b						
FT mat_peptide	-61..399						

```

FT      /tab- c
FT      misc_feature 61..129
FT      /tag= d
FT      /label= FR1
FT      misc_feature 130..180
FT      /tag= e
FT      /label= CDR1
FT      misc_feature 181..225
FT      /tag= f
FT      /label= FR2
FT      misc_feature 226..246
FT      /tag= g
FT      /label= CDR2
FT      misc_feature 247..342
FT      /tag= h
FT      /label= FR3
FT      misc_feature 343..369
FT      /tag= i
FT      /label= CDR3
FT      misc_feature 370..399
FT      /tag= j
FT      /label= FR4
FT      EP-686696-A1.
FT      13-DEC-1995.
FT      09-JUN-1995; 201535.
FT      09-JUN-1994; CU-000073.
FT      (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
FT      (KAMB/) KAMBEEL R W.
FT      Ayala Avila MA, Canaan-Haden Frias LM; del Carmen Dominguez Horta MC;
FT      Fernandez de Cossio Dorta-Duque ME, Gavilondo Cowley JVG;
FT      WPI; 96-021914/03.
FT      P-PSDB; R85909.
FT      New recombinant single chain Fv antibody fragment - useful for
FT      immuno-purification and detection of HBSAg
FT      Claim 1; Page 19; 23pp; English.
FT      CC 074066 and 074067 encode the heavy and light chain variable domains of
FT      the murine hybridoma-derived monoclonal antibody CB-Hep.1 Fv region.
FT      CC The heavy and light chain regions are used to produce a recombinant
FT      CC antibody fragment having specificity for the hepatitis B virus
FT      CC surface antigen (HBSAg). The recombinant antibody may be used for
FT      CC immunopurification of HBSAg, in immunoassays for the detection of
FT      CC HBSAg and for insolubilisation of heterologous fusion proteins
FT      CC expressed in E. coli aiding their purification.
FT      CC Sequence 399 BP; 98 A; 88 C; 101 G; 112 T;
SQ
Query Match 72.9%; Score 288.6; DB 1; Length 399;
Best Local Similarity 84.5%; Pred. No. 1.1e-85;
Matches 337; Conservative 0; Mismatches 59; Indels 3; Gaps 1;
QY 1 atggtttacacagggccaggtttctatatgtcgtcgtcgtatggtatctgcacccgtgag 60
DB 1 ATGGATTACACAGGCCAGGTTCTTATGTTACTGCTGTAATGGTAATCTGTGACTGTGGG 60
QY 61 gacattgctcacacagctccagatccctgcgtcgtgaattgaggagagggccact 120
DB 61 GACATTGTAATCTACAGCTCTCATCTCCCTAAGCTGTGTAAGTAAGAGTGGT 120
QY 121 attagctgaacatccagtcagtcgtcctcaacagtagaacccgagaagaactactgct 180
DB 121 TTGACTGCAAGTCCAGTCTAGAGTCTTTATATCTTAACAAACACAGAACTACTGGGC 180
QY 181 tgggtaccagcagaacacagggcagcctcctaaactcgtatcactggcgtacactag 240
DB 181 TGGTTCACAGCAAAACCTGGGCAAGTCTCTAAACTGCTATTTACTGGGCATCCACTAG 240
QY 241 gaattggaggtccctgattcgtcgtcagtcagtcagtcagtcagtcagtcagtcagtc 300
DB 241 GATTGTGGGGTCCCTGATCGCTTTCACAGGCAAGTGAATCTGGGACAAATTCATCTCAG 300
QY 301 atcagcagctctgcagcgtctgaagcgtctgagcgttactactgacgcaactctata---at 357
DB 301 ATCAGCAGGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTGCAACAAATATATATTAT 360

```

```

QY 358 cttaacgttcgacaggggacccaaggttggaataaaaa 396
DB 361 CCGTACAGCTTCGGAGGGGACCAAGCTGGAAATYAAA 399
RESULT 8
T60734
ID T60734 standard; cDNA; 439 BP.
AC T60734.
DT 25-SEP-1997 (first entry)
DE cDNA encoding wild type murine anti-E-selectin antibody Cy1787(L).
KW Humanised; murine; mouse; E-selectin; antibody; light chain;
KW variable region; detection; inhibition; mediation; cell adhesion;
KW diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
KW acute respiratory distress syndrome; gross cystic breast disease;
KW cancer; treatment; splanchic occlusion shock; psoriasis;
KW complement; ds.
OS Mus spp.
FT Key Location/Qualifiers
FT cds 16..426
FT /tag= a
FT /note= "no stop codon given"
FT WO9640942-A1.
FT 19-DEC-1996.
FT 06-JUN-1996; U09204.
FT 07-JUN-1995; US-482112.
FT (CYTE-) CYTEL CORP.
FT PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;
FT PI Jones S;
FT DR WPI; 97-077272/07.
FT P-PSDB; W10547.
FT Humanised anti-E-selectin antibody - useful for diagnosis and
FT treatment of, e.g. inflammatory responses, septic shock, acute
FT PT respiratory distress syndrome or cancer
FT CC Example II; Page 55; 89pp; English.
FT CC The present sequence encodes the wild type murine anti-E-selectin
FT CC antibody (Ab) light chain variable region, Cy1787(L), which was
FT CC used in the preparation of the humanised anti-E-selectin Ab light
FT CC chain variable regions, Cy1788V(LA-B). The humanised Ab can
FT CC be used to detect E-selectin, or inhibit E-selectin mediated cell
FT CC adhesion. They can also be used to diagnose, reduce or inhibit an
FT CC inflammatory response, or the severity of pathologies, e.g. septic
FT CC shock, acute respiratory distress syndrome, wound associated
FT CC sepsis, gross cystic breast disease or cancer, or treat, e.g.
FT CC splanchic occlusion shock, or psoriasis. They can be administered
FT CC to a human without inducing an immune response, in addition, the
FT CC effector portion of the Ab can interact with various components of
FT CC the human immune system, including complement.
FT CC Sequence 439 BP; 108 A; 110 C; 116 G; 105 T;
SQ
Query Match 72.9%; Score 288.6; DB 1; Length 439;
Best Local Similarity 84.5%; Pred. No. 1.1e-85;
Matches 337; Conservative 0; Mismatches 59; Indels 3; Gaps 1;
QY 1 atggtttacacagggccaggtttctatatgtcgtcgtcgtatggtatctgcacccgtgag 60
DB 1 ATGGATTACACAGGCCAGGTTCTTATGTTACTGCTGTAATGGTAATCTGTGACTGTGGG 60
QY 28 ATGAGAGTACACAGACGTCTCATCTCCCTGATGTCCTGTTGGTAATCTGTGACTGTGGG 87
DB 28 ATGAGAGTACACAGACGTCTCATCTCCCTGATGTCCTGTTGGTAATCTGTGACTGTGGG 87
QY 61 gacattgctcacacagctccagatccctgcgtcgtgaattgaggagagggccact 120
DB 61 GACATTGTAATCTACAGCTCTCATCTCCCTGATGTCCTGTTGGTAATCTGTGACTGTGGG 120
QY 121 attagctgaacatccagtcagtcgtcctcaacagtagaacccgagaagaactactgct 180
DB 121 TTGACTGCAAGTCCAGTCTAGAGTCTTTATATCTTAACAAACACAGAACTACTGGGC 180
QY 181 tgggtaccagcagaacacagggcagcctcctaaactcgtatcactggcgtacactag 240
DB 181 TGGTTCACAGCAAAACCTGGGCAAGTCTCTAAACTGCTATTTACTGGGCATCCACTAG 240
QY 208 TGGTACACAGCAAAACCTGGGCAAGTCTCTATCTGTTGATCTACTGGGCACTCAGG 267
DB 208 TGGTACACAGCAAAACCTGGGCAAGTCTCTATCTGTTGATCTACTGGGCACTCAGG 267
QY 241 gaattggaggtccctgattcgtcgtcagtcagtcagtcagtcagtcagtcagtcagtc 300
DB 241 GATTGTGGGGTCCCTGATCGCTTTCACAGGCAAGTGAATCTGGGACAAATTCATCTCAG 300

```

```

Db      268 GAAATCGGGGTCCTCGATGCTTCACAGGACGTGATCTGGAACAGATTCTACTCTCAC 327
      301 atcagcagctctcagcgtcgaagcgtgcagcttattactgcagcaatctata--at 357
      328 ATCAGCAGCTCTGACAGGCTGGAACCTGGCAGTTATTACTGTGAGATGATATATATTAT 387
      358 cttacacgcttcggacaggggacgaaggtggaataaaa 396
      388 CCGCTCACGTTCCGTGCTGCTGGGACCAAGGTGAGACTGAAA 426

```

```

RESULT 9
ID      T34152
AC      T34152 standard; DNA; 418 BP.
DT      14-FEB-1997 (first entry)
DE      Monoclonal antibody PA1-3F10 variable light chain-encoding DNA.
KW      PA1-3F10; antibody; hybridoma; BCMB1322CB; cancer; target; epitope;
KW      killing; colorectal; lung; ovary; cytotoxin; neoplasia; ss.
OS      Mus musculus.
FH      Key
FT      Location/Qualifiers
      2..418
      /tag= a
      /note= "no start or stop codon"

```

```

PD      25-JUL-1996.
PE      15-JAN-1996; SE0029.
PR      18-JAN-1995; SE-000148.
PI      (BIOT-) BIOINVENT INT AB.
PI      Carlsson R, Jansson B;
DR      WPI: 96-354478/35.
DR      P-PSDB: R99469.
PT      Monoclonal antibody PA1-3F10 produced by hybridoma BCMB1322CB -
PT      useful to target cancer cells for killing or detection
PS      Claim 10; Fig 10; 62pp; English.
CC      T34152 encodes the variable light (VL) chain of monoclonal antibody
CC      PA1-3F10 produced by hybridoma BCMB1322CB. The antibody is
CC      directed against an epitope present on cancer cells, in particular
CC      breast, ovary, lung and colorectal cancer cells. The antibody is
CC      useful for detecting cancer cell epitopes and hence in the diagnosis
CC      of cancer. The antibody can be conjugated to a cytotoxic compound and
CC      targeted to cancer cells to kill them.
SQ      Sequence 418 BP; 102 A; 100 C; 107 G; 109 T;

```

```

Query Match      72.4%; Score 286.8; DB 1; Length 418;
Best Local Similarity 84.8%; Pred. No. 4.4e-85;
Matches 334; Conservative 0; Mismatches 57; Indels 3; Gaps 1;

```

```

OY      6 ttcacagagccaggtcttattatctgctgcgtatggtatctggcacctgtggagacat 65
      1 TTACACAGGCCACAGTTCTTATGTTACTGCTGCTATGGGTTATGTTACCTGTTGGGACAT 60
OY      66 tgtctgacacagctctccagatccctgctgtaagcttagagagagggccaattag 125
      1 TGGAGTGTACAGTCTCCACATCTCCCTAGCTGTGTGAGAGAGAGTTACTATAAC 120
Db      61 TGGAGTGTACAGTCTCCACATCTCCCTAGCTGTGTGAGAGAGAGTTACTATAAC 120
OY      126 ctgcaaatcagctcagatgtctcaacagtagaaccggagagaactactgtgcttgta 185
      121 CTCAGATCTCAGTCCAGTCAAGGCTTTTATATATAGTACCAATCAAAAGAACTATGGCTGGTA 180
Db      121 CTCAGATCTCAGTCCAGTCAAGGCTTTTATATATAGTACCAATCAAAAGAACTATGGCTGGTA 180
OY      186 ccagcagaacacccagagcagcctcctaactgctgacttactgtggcactcactgggaatc 245
      181 CCAGCAGAAACAGGCGCAGTCTCTTAACCTGCTGATTTACTTGGGCACTCCCTAGGGAATC 240
Db      181 CCAGCAGAAACAGGCGCAGTCTCTTAACCTGCTGATTTACTTGGGCACTCCCTAGGGAATC 240
OY      246 tggggctccctgactcgtctcagttgagcagtgatctggagacagattcacttcacatcag 305
      241 TGGGGTCCCTGATGCTTTCACAGGCACTGATCTGGGAGAGATTTCCTCAGCAGATCAG 300
Db      241 TGGGGTCCCTGATGCTTTCACAGGCACTGATCTGGGAGAGATTTCCTCAGCAGATCAG 300
OY      306 cagctcgcagagctcgaagagcttgacagtttatctacgcagcaatctat--aatctta 362
      301 CAGTGTGAAAGCTGAAAGACCTGGCAGTTTATCTGTCACCAATATTATGCTATCTCG 360
Db      301 CAGTGTGAAAGCTGAAAGACCTGGCAGTTTATCTGTCACCAATATTATGCTATCTCG 360

```

```

OY      363 cagcttcggacaggggacgaaggtggaataaaa 396
      361 GACGTTCCGTTGAGAGCCAGCAGCTGGAATCAAA 394
Db      361 GACGTTCCGTTGAGAGCCAGCAGCTGGAATCAAA 394

```

```

RESULT 10
ID      T72268
AC      T72268 standard; cDNA; 439 BP.
DT      03-JAN-1998 (first entry)
DE      Chimeric MAb 15 PCR-modified light chain variable region cDNA.
KW      Humanised antibody; monoclonal antibody; MAb 15; tumour;
KW      lung cancer; therapy; ds.
OS      Chimeric mus musculus.
FH      Key
FT      Location/Qualifiers
      16..187
      /tag= a
      /tag= b
      mat_peptide 88..1426
      /tag= b

```

```

PD      EP-781847-A1.
PN      02-JUL-1997.
PE      25-OCT-1996; 117154.
PR      06-NOV-1995; EP-117407.
PI      (MERE) MERCK PATENT GMBH.
PI      Bendig M, Jones T, Saldana J;
DR      WPI: 97-334904/31.
DR      P-PSDB: W21655.
PT      Humanised form of murine monoclonal antibody MAb 15 - useful for
PT      treating lung cancer;
PT      Disclosure; Fig 4; 71pp; English.
CC      This cDNA sequence comprises the light chain variable region VL
CC      sequence of murine monoclonal antibody (MAb) 15 (DSM ACC2117),
CC      modified for the expression of chimeric 15 antibody. The 5' and
CC      3' ends of the VL sequence (see also T72238) were modified by
CC      PCR (see T72243-44) to provide a kozak sequence for efficient
CC      translation, a 5' HindIII site for cloning into HCV vectors, a
CC      3' splice donor site at the J-C junction for splicing the mouse
CC      variable regions to human constant regions and a 3' BamHI site for
CC      cloning into HCV vectors. The VH sequence was similarly modified
CC      (see T72269). The modified VL and VH sequences were used in a
CC      claimed process to model and design novel humanised, reshaped MAb
CC      15 having humanised, reshaped VL and VH sequences (see W21651 and
CC      W21652), which can be used for treating tumours, especially lung
CC      cancer, and for the manufacture of a drug related to tumours,
CC      especially lung cancer.
SQ      Sequence 439 BP; 109 A; 107 C; 112 G; 111 T;

```

```

Query Match      72.1%; Score 285.4; DB 1; Length 439;
Best Local Similarity 84.0%; Pred. No. 1.3e-84;
Matches 335; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

```

```

OY      1 atgattccagggccaggtcttattatctgctgctgtaaggatctggcacctgtgg 60
      28 ATGAGACTCACAGACCTGTTGTTTATGTTACTGCTGCTATGGGTTATGTTACCTGTTGGG 87
Db      28 ATGAGACTCACAGACCTGTTGTTTATGTTACTGCTGCTATGGGTTATGTTACCTGTTGGG 87
OY      61 gacatgtgtctgacacagctccagatccctgctgctgttaagcttagagagagggccact 120
      88 GACATGTTGATGTACACAGTCTCCATCTCCCTAGCTGTGTCTGAGTGGAGAGAGTTACT 147
Db      88 GACATGTTGATGTACACAGTCTCCATCTCCCTAGCTGTGTCTGAGTGGAGAGAGTTACT 147
OY      121 atgaagtgcaaatccagctcagatgtctgcacacagtagaaccggagagaactacttgct 180
      148 ATGAGCTGCAAGTCCAGTCTAGACCTTTTATATAGTAGCAATCAAAAGAACTACTTGGCC 207
Db      148 ATGAGCTGCAAGTCCAGTCTAGACCTTTTATATAGTAGCAATCAAAAGAACTACTTGGCC 207
OY      181 tggctacacagaacacccagggcagcctcctaactgctgacttactgtggcactcactagg 240
      208 TGGTACACAGAGAAACAGGCGAGTCTCTTAACAGCTGATTTACTTGGGCACTCAGTAGG 267
Db      208 TGGTACACAGAGAAACAGGCGAGTCTCTTAACAGCTGATTTACTTGGGCACTCAGTAGG 267
OY      241 gaactcggggtccctgactcgtctcagttcagtgagcagtgatctggagacagattcactcacc 300
      268 GAATCTGGGGTCCCTGATGCTTTCACAGGCACTGATCTGGGAGAGATTTCACCTCACC 327
Db      268 GAATCTGGGGTCCCTGATGCTTTCACAGGCACTGATCTGGGAGAGATTTCACCTCACC 327

```

QY	301	atccagcctcgcagcagcgcgaagcgtgacgttttcttactgcagccatctatc	---	at	357
Db	328	ATCAGCAGCGTGAAGGCTGAGAGACCCGGCAGTTTATTACTGCACGATATTCTA	CTAT	387	
QY	358	cttaccagcttcgcagcagggaccacaaaggttgagataa	396		
Db	388	CCTCGACGCTTCGGTGGAGGACCAAGCTGGAAATCAAA	426		
RESULT	11				
TT72238					
AC	TT72238	standard; cdna; 460 BP.			
DT	03-JAN-1998	(first entry)			
DE	Mouse MAB 15 light chain variable region CDNA.				
DE	Humanised antibody; monoclonal antibody; MAb 15; tumour;				
KW	Lung cancer; therapy; ds.				
OS	Mus musculus.				
FH	Key	Location/Qualifiers			
FT	sig_peptide	1..72			
FT	mat_peptide	/*tag= a			
FT		73..411			
FT		/*tag= b			
PN	EP-781847-A1.				
PD	02-JUL-1997.				
PF	25-OCT-1996.	117154.			
PR	06-NOV-1995.	EP-117407.			
PA	(MERE) MERCK PATENT GMBH.				
PI	Bendig M, Jones T, Saldana J;				
PI	WPI; 97-334904/31.				
DR	P-PSDB: W21653.				
PT	Humanised form of murine monoclonal antibody MAb 15 - useful for				
PT	treating lung cancer				
PS	Claim 14; Fig 1; 71pp; English.				
CC	This CDNA sequence encodes the light chain variable region VL				
CC	(W21653) of murine monoclonal antibody (MAb) 15 (DSM ACC2117),				
CC	a MAb that shows a therapeutic effect on human tumour cells,				
CC	especially human lung cancer. The clone was isolated from				
CC	hybridoma CDNA using a degenerate leader sequence primer (T72233)				
CC	and a kappa constant region reverse primer (T72240). The VH region				
CC	(see T72267) was also amplified. The VL and VH sequences were				
CC	used in a claimed process for the production of novel humanised,				
CC	reshaped MAb 15 having humanised, reshaped VL and VH sequences				
CC	(see W21651 and W21652), which can be used for treating tumours,				
CC	especially lung cancer, and for the manufacture of a drug related				
CC	to tumours, especially lung cancer.				
SO	Sequence 460 BP; 112 A; 118 C; 113 G; 117 T;				
Query Match	72.1%;	Score 285.4;	DB 1;	Length 460;	
Best Local Similarity	84.0%;	Pred. No. 1.3e-84;			
Matches	335;	Conservative 0;	Mismatches 61;	Indels 3;	Gaps 1.
QY	1	atggaattcagcagccaggttcttatatctctcgtcgtatggtatctgcacacctgtgg	60		
Db	13	ATGGAATTCACATCTCCCTGGTCTTATGTACTGCTGCTAGTGATCTGTACTGCTG	72		
QY	61	gacatctgctgcagcagctctcgaattccctcgtcgttaagcttgagagagggccact	120		
Db	73	GACATCTGTATGTCAACAGCTCCATCTCTCCCTAGCTGTCTCAGTTGGAGAGAGTT	132		
QY	121	attagctcgaatcagctagtagctctctcacaagtagaacccggagagaactacttgct	180		
Db	133	ATGACTTCGAATCCAGTCCAGTCCAGTCCCTTTATATAGTAGCAATCAAAAGACTT	192		
QY	181	tgttaccagcagaaccagcagcagcctccttaactctgatacttactggtgcattcct	240		
Db	193	TGTTGTCACGACAAACACAGGCGCAGTCTCTTAACAGCTGATTTTACGGCATC	252		
QY	241	gaatctgggtgtccctgattgcttgaagtgtagtgatctggagacagattactctcacc	300		
Db	253	GAATCTGGGTGTCCCTGATTCGCTTACAGGCAATGTGGAGCAAGATTTCCTCTCACC	312		

```

0Y 301 atcagcagctctcagcagcggaagagctgacgtttatctctcagcgaactctata---at 357
Db 313 ATCCACAGAGGTAAGAGCGTGAAGACCCGCGAGTTTATCTGTCAGCAATATTCTACTAT 372
0Y 358 cttaacgcttcgacagaggagaccaaaggtggaataa 396
Db 373 CCTCGAGCTTGCGTGGAGGCGCACCAAGCTGGAATCAAA 411

RESULT 12
X34465
X34465 standard: cDNA; 342 BP.
X34465:
DE 25-JUN-1999 (first entry)
DE Mouse MAB 6A4 light chain variable region encoding DNA.
KW Rolling template; nucleic acid synthesis; polynucleotide polymerase;
KW gene production; primer; monoclonal antibody; 6A4; ss.
OS Mus sp.
PN MO9914370-A1.
PD 25-MAR-1999.
PF 15-SEP-1998; U19157.
PR 15-SEP-1997; US-929856.
PA (HINT/) HIAT F D.
PA (ROSE/) ROSE F D.
PI Hiatt AC, Rose PD;
PI WPI: 99-244045/20.
DR P-BDB: 106830.
PT Producing specific polynucleotides using rolling templates
PS Example 6; Page 40; 109pp; English.
SS The invention relates to a method for producing polynucleotides having a
CC defined sequence using rolling templates that successively add
CC nucleotides (nts) to a longer primer strand. The method comprises: (1)
CC incubating, under annealing conditions, a primer and a template that has
CC a 5'-region not complementary to the primer, a 3'-region complementary to
CC the 3'-end of primer and a non-reactive 3'-terminus, with the template
CC being shorter than the primer; (ii) reacting the primer with at least one
CC nt in presence of a template-dependent polynucleotide polymerase to
CC extend it by at least one nt (complementary to the 5'-region of template)
CC at its 3'-end; (iii) separating the template and the extended primer; and
CC (iv) repeating the cycle of (i)-(iii) as often as needed to synthesize
CC the desired polynucleotide. The method is especially used to produce
CC genes or their segments. The method provides fast, accurate, inexpensive
CC synthesis of RNA or DNA and is more efficient than chemical coupling
CC processes. It has higher specificity and eliminates the need for
CC deprotection. The products can be cloned directly. The method avoids
CC problems of waste disposal and includes an inherent editing effect
CC (false sequences will not be extended further in subsequent rounds) so
CC that purification of the end product is facilitated. Synthesis may take
CC place on a vector, simplifying cloning and sequences with codon usage
CC optimized for a particular host can be prepared. This represents the
CC nucleotide sequence of the light chain variable region of the mouse
CC monoclonal antibody (Mab) 6A4, synthesised by the method of the
CC invention.
CC
CC Sequence 342 BP; 88 A; 87 C; 87 G; 80 T;
SQ

Query Match 71.5%; Score 283.2; DB 1; Length 342;
Best Local Similarity 90.2%; Fred. No. 6.1e-84;
Matches 303; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

0Y 61 gacattgtctacacagctcagatcccgctgctgaagtttagggagagggcact 120
Db 1 GACATTGTGATGTATCACAAGCTCTCAATCCCTCCGCTGTGTACGACGAGAGAGAGTCACT 60
0Y 121 attagctgcaaatccagtcagatcagctgtctcaacagtagaaccggagagaaactattgct 180
Db 61 ATGAGCTGCAAAATCCAGTCAGAGCTGTGCTCAACAGTATAAACCCGAAAGAACTTTGGCT 120
0Y 181 tggtcacagcagaaccggagcagctctcttaacatgcgtatctattggtcatcactg 240
Db 121 TGGTACCAAGCAAAACCAAGGCGCATGCTCTTAACATGCTGATCTACTGTGGCATCCACTAGG 180

```

QY 241 gaatctgggtccctgacgtcttcagctgagctgagctgagcaattcactctacc 300
DB 181 GAATCTGGGGTCCCTGATCGTTTCACAGCGAGTGGGACGATTCACCTCCTCAC 240
QY 301 atcagcagctctgcaagcttgaagacgttgcagcttattactgacgcaatctatactt 360
DB 241 ATCAGCAGTGTGACAGGCTGACAGCTGCGCAGTTTATTACTGCAAGCAATCTTAACTCT 300
QY 361 tacagcttcgagcaggaggaccagaagtggaaataaaa 396
DB 301 CGAGCGTTGGGTGGAGGACCAAGCTGAAATCAAA 336

RESULT 13

Q62958
ID 062958 standard; DNA: 1443 BP.
AC 062958;
DT 09-SEP-1994 (first entry)
DE Glycophorin antibody 1C3 Fab coding region.
KW Glycophorin; antibody 1C3; target binding polypeptide; PCR;
KW polymerase chain reaction; primer; antibody engineering;
KW humanized antibody; phagemid pHFA; plasmid p569;ss.
OS Synthetic.
PN WO9407921-A.
PD 14-APR-1994.
PF 24-SEP-1993: AU00491.
PR 25-SEP-1992: AU00491.
PA (CSTR) COMMONWEALTH SCI & IND RES ORG.
PI Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;
PI Lah M, Malbyrl, Power BE;
DR WPI: 94-135515/16.
PT New target-binding polypeptide(s) used for diagnosis, etc. -
PT having a stable core polypeptide region with at least one
PT target-binding region covalently attached, opt. mutated to alter
PT specificity, etc.
PS Disclosure: Page 42; 67pp; English.
CC PCR primers given in 062951-52 were used to clone anti-glycophorin
CC antibody 1C3 Fab coding region. The DNA sequence of the first 1443
CC bases of the Fab fragment in pHFA, ready for ligation post PCR
CC amplification for ligation into p569, is given in 062958.
SQ Sequence 1443 BP; 391 A; 388 C; 351 G; 313 T;

Query Match 70.7%; Score 279.8; DB 1; Length 1443;
Best Local Similarity 84.6%; Pred. No. 1.4e-82;
Matches 314; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 26 tatctgctgctatggtatctggtacactgtggtgacattgtctgacagctccag 85
DB 734 TCTTACCGTTACTGTTTACCCCGGTAAACCAAGCCGACATCGTCATGTCACAGTCCAT 793
QY 86 attccctgctctaagcttaagagagagagggccactattgctgcaaatccagtcagatc 145
DB 794 CCTCCCTGCTGTGTCAGTAGAGAGAAAGTCTCATGTGAGCTGCAGATCAGACAGTTC 853
QY 146 ttgtctcaagctgaagaccgaagaactactgttgctgtgacagcagaacccaaggcagc 205
DB 854 TGTTCACAGTGAACCCCAAGAACTACTGTGCTGTGTAACAGCAAGCAAGGAGCACT 913
QY 206 ctctcaaatctgcatctactggtgacatccactaggaatctgggtgctcctgactgctta 265
DB 914 CTCCTAAACCGGTGATCTACTGTGGCATTCACATGAGGAATCTGGGGTCCCTGATCGTTCA 973
QY 266 gtggcagctgcatctggaagagatttcaactcacaacacagcagctgtcaggtgaaagc 325
DB 974 CAGGCGAGTGTGAGAGAGATTTCATCTCACATCAGCAGTGTGCGAGGCTGAGAGACC 1033
QY 326 ttggcagcttattactgacgcaatctataatcttaacagcttcgagcaggaggacaaag 385
DB 1034 TGGCAGATTATTACTGCAAGCAATCTTAACTCTGCAAGCTTGGTGGAGGACCAAGC 1093
QY 386 tggaaataaaa 396
|||||

DB 1094 TGGAAATTAA 1104

RESULT 14

V36237
ID V36237 standard; DNA: 747 BP.
AC V36237;
DT 08-SEP-1998 (first entry)
DE DNA of ScFv D3M which binds to mutant p53 proteins.
KW Single chain antibody; ScFv D3M; mouse; p53 protein; oligomerisation;
KW regulatory domain; p53 mutant; H273; W248; G281;
KW p53-dependent trans-activating activity; restoration;
KW tumour-suppressing activity; tumour cell; treatment;
KW hyper-proliferation; cancer; re-stenosis; ss.
OS Mus SP.
PN WO9818625-A1.
PD 07-MAY-1998.
PF 27-OCT-1997: F01921.
PR 29-OCT-1996; FR-013176.
PA (RHON) RHONE-POULENC RORER SA.
PI Debussche L, Bracco L;
DR WPI: 96-272140/24.
DR P-PSDB; W60770.
PT Restoring p53-dependent trans-activating activity to cell containing
PT mutant p53 - by delivering single-chain antibody specific for the
PT mutant, particularly for treatment of tumours
PS Claim 5; Page 32; 54pp; French.
CC The present sequence encodes a single chain antibody (ScFv) designated
CC D3M. The antibody binds to an epitope present in the C-terminal region
CC of the p53 protein that includes oligomerisation and regulatory domains,
CC specifically between positions 320 and 393. ScFv D3M is directed against
CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
CC introduced into cells containing a mutant p53 protein, p53-dependent
CC trans-activating activity is restored. ScFv D3M is specific for
CC p53-mutants that have lost tumour-suppressing activity and are present in
CC tumour cells. It is particularly used to treat hyper-proliferation
CC associated with these mutants (e.g. cancer and re-stenosis) but may also
CC be used in vitro for studying mechanisms of activity of p53 or its mutant
CC and to purify or detect p53.
SQ Sequence 747 BP; 189 A; 188 C; 205 G; 165 T;

Query Match 70.2%; Score 277.8; DB 1; Length 747;
Best Local Similarity 89.0%; Pred. No. 5e-82;
Matches 300; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 60 ggacactgtgtgacacagctccagattccctggtctgtaagcttagagagagggccac 119
DB 411 GGACATTGAGTGCACCCAGTCTCCATCTTCCCTGCTGTGACAGAGAGAAAGGTGCG 470
QY 120 tattagctgcaaatccagtcagagctctctcaacagtgaaaccggaggaactacttggc 179
DB 471 TATGAGCTGCAATCACTCAAGTCTGTTCAACAGTGAACCCCAAGAAATTACTTGGC 530
QY 180 ttgtgacacagcaagcaggcagccctcaaatgtgtgacttactggtgaatccactag 239
DB 531 TTGGAATCAGCAAGAAACAGGAGCACTCTTAAGTGTGATCTACTGGCATCCACTAG 590
QY 240 ggaatctgggtccctgtactgcttcagctgagctgagctgggaagattcaactctcac 299
DB 591 GGAATCTGGAGTCCCTGATTCGCTTCACAGGCGAGTGGAGTTCACATCTCCTCAC 650
QY 300 catcagcagctctgcaagctggaagcgtggcagcttataactgacgcaatctataact 359
DB 651 CATCAGCAGTGTGCAAGGCTGAAGACCTGCGAGTTTATTACGCAAGCAATCTTAACTCT 710
QY 360 ttacagcttcgagcaggaggccaaggtggaataaaa 396
DB 711 ACCGACGTTTCGGCGGGGACCAAGCTGGAATCAAA 747
RESULT 15
Q62956

ID Q62956 standard; DNA; 870 BP.
AC Q62956;
DT 09-SEP-1994 (first entry)
DE Glycophorin antibody 1C3 scfv.
KW Glycophorin; antibody 1C3; target binding polypeptide; PCR;
polymerase chain reaction; primer; scfv; single chain antibody;
phagemid pHEA; vector; antibody engineering; humanized antibody;
ss.
OS Not specified.
PN WO9407921-A.
PD 14-APR-1994.
PF 24-SEP-1993; AU0491.
PR 25-SEP-1992; AU-004973.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PI Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;
PI Lah M, Malbyrl, Power BE;
PI WPI: 94-135515/16.
DR P-PSDB; R52864.
PT New target-binding polypeptide(s) used for diagnosis, etc.
PT having a stable core polypeptide region with at least one
PT target-binding region covalently attached, opt. mutated to alter
PT specificity, etc.
PS Disclosure, Page 40; 67pp; English.
CC PCR primers N2034 (Q62947) and N2035 (Q62948) were used with anti-
CC glycophorin 1C3 antibody template DNA in a PCR to produce a 1C3
CC product of 3'-VH sequence juxtaposed to 5'-VL sequence flanked by
CC BstEII and NotI sites. Products were ligated with vector pHEA
CC containing a 1C3 scfv sequence, and expressed in Escherichia coli
CC TGI. The DNA sequence of the linkerless 1C3 scfv in pHEA is given
CC in Q62956 (encoding protein R52864).
SQ Sequence 870 BP; 236 A; 205 C; 226 G; 203 T;

Query Match 69.6%; Score 275.8; DB 1; Length 870;
Best Local Similarity 89.0%; Pred. No. 2.4e-81;
Matches 298; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 61 gacatgtgctgcacacacatccagatccctgctgtaagcttagagagagagccact 120
DB 463 GACATGCTGCATGTCACATGTCATCCCTCGCTGTCTCAGTAGAGAGAGTCACT 522
QY 121 attagctgaataatccagtcagatgctgtcaacagtagaacccgagaaactacttgct 180
DB 523 ATGAGCTGCAAGATCCAGTCAAGATGTTTCAACAGTAGAACCCGAAAGAACTACTT 582
QY 181 tggtaaccagcgaacccagcagctcctaactgctgactactggtgcatccactagg 240
DB 583 TGGTACCGACGAGAAACGAGGCGAGTCTTAACCGCATCTACTGGGCACTCCACTAGG 642
QY 241 gaactggggctccctgactgcttcagtgagcagtgatggagacagatttcaactacc 300
DB 643 GAATCTGGGGTCCCTGATCGCTTCACAGGCGAGTGGATCTGGGACAGATTTCCTCACC 702
QY 301 atcagcagctcgcagcagctgaagacgtgagcagttatctactgacgcgaactctatactt 360
DB 703 ATCAGCAGGTGTGAGGCGTGAAGACCTGACAGATATTAATCTGCAAGCAATCTTAATCTT 762
QY 361 tacacgttcggagcagggagaccaggttggaaataa 395
DB 763 CGGACGTCGCTGGAGGCGACCAAGCTGGAATTA 797

Search completed: August 27, 2000, 06:25:36
Job time: 1933 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 06:24:06 ; Search time 56.18 Seconds

(without alignments)
969.600 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396

Sequence: 1 atgagttacacagccaggt.....ggacacagtggaataa 396

Scoring table: IDENTITY_NNC

Gapop 10.0 , Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	83.8	940	1	US-08-353-400-24
2	279.8	70.7	1443	3	US-08-403-853-19
3	277.4	70.1	399	6	PCT-US93-11611-1
4	275.8	69.6	870	3	US-08-403-853-15
5	267.2	67.5	1701	3	US-07-916-098A-54
6	267.2	67.5	1701	3	US-07-916-098A-55
7	264.6	66.8	327	4	US-08-308-494A-24
8	264.6	66.8	399	6	PCT-US93-11612-1
9	248.2	62.7	344	3	US-07-916-098A-34
10	247	62.4	5703	1	US-08-467-420A-50
11	247	62.4	5703	2	US-08-470-110A-50
12	247	62.4	5703	2	US-08-667-769A-50
13	247	62.4	5703	3	US-08-940-371-50
14	247	62.4	5703	6	PCT-US93-17082A-50
15	241.6	61.0	336	3	US-07-916-098A-14
16	241.6	61.0	339	5	US-08-483-749A-15
17	241	60.9	340	3	US-07-916-098A-13
18	238.6	60.3	795	4	US-08-822-028-11
19	238.2	60.2	342	4	US-08-428-257A-75
20	233.4	58.9	339	6	PCT-US93-08435-3
21	232.8	58.8	924	4	US-08-860-174A-9
22	232.6	58.7	1706	4	US-08-860-174A-11
23	231.8	58.5	999	4	US-08-860-174A-6
24	230.2	58.1	339	1	US-08-442-542-11
25	230.2	58.1	339	5	US-08-765-469-11
26	229.8	58.0	1088	5	US-08-463-903-3

27	228.2	57.6	836	3	US-08-933-616-1	Sequence 1, Appl
28	227	57.3	339	1	US-08-442-542-46	Sequence 46, Appl
29	227	57.3	339	5	US-08-765-469-46	Sequence 46, Appl
30	227	57.3	342	2	US-08-360-125-4	Sequence 4, Appl
31	227	57.3	342	2	US-08-450-578-4	Sequence 4, Appl
32	227	57.3	342	4	US-09-017-628-4	Sequence 4, Appl
33	227	57.3	342	4	US-09-014-880-4	Sequence 4, Appl
34	226.4	57.2	856	5	US-08-463-903-16	Sequence 16, Appl
35	226.4	57.2	877	5	US-08-463-903-14	Sequence 14, Appl
36	226	57.1	1330	5	US-08-463-903-5	Sequence 5, Appl
37	226	57.1	1331	5	US-08-463-903-7	Sequence 7, Appl
38	226	57.1	1346	5	US-08-463-903-9	Sequence 9, Appl
39	226	57.1	1352	5	US-08-463-903-11	Sequence 11, Appl
40	224.4	56.7	339	3	US-08-263-911-1	Sequence 1, Appl
41	224.4	56.7	1027	5	US-08-463-903-19	Sequence 19, Appl
42	224.4	56.7	2165	3	US-08-263-911-6	Sequence 6, Appl
43	224.4	56.7	2165	3	US-08-263-911-8	Sequence 8, Appl
44	223	56.3	360	1	US-08-026-320A-3	Sequence 3, Appl
45	222.4	56.2	803	2	US-08-323-445A-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-08-353-400-24
Sequence 24, Application US/08353400
Patent No. 3663357
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 940 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-353-400-24

Query Match      83.8%, Score 332, DB 1, Length 940;
Best Local Similarity 89.9%, Pred. No. 1e-97;
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 atgagttacacagccaggtcttatgtctgcgtcattggtatctggcaccctgtgg 60
   |||||||
DB 10 atgagttacacagccaggtcttatgtctgcgtcattggtatctggcaccctgtgg 69
   |||||||
QY 61 gacattgtcgtacacacattccacattccctgtgtgaagcttagagagagagccact 120
   |||||||
DB 70 gacattgtcgtacacacattccacattccctgtgtgtcagcagagagagagctacc 129
   |||||||
QY 121 attagctcaaatccagtcagagtcgtctcaacagtagaacccgagagaaacttggct 180
   |||||||
DB 130 atgacctcaaatccagtcagagtcgtctcaacagtagaacccgagagaaacttggct 189
   |||||||
```

	Matches	314:	Conservative	0:	Mismatches	57:	Indels	0:	Gaps	0:
OY	26	tattgctcgtctataggtatcttgcacccgttgaggacaattgctgaacacagtctccag								85
Db	734	TCTTACCCGTACTCTTTATGACCCTCGGTAAACCAAGCCGACATCGTCATGTGCACAGTCTCCAT								793
OY	86	attcccctgcgttaagtccttagagaagagggccactattagctcgcaaatccaaagtcagctc								145
Db	794	CCTCCTTGCTGGCTGTGTGTCATAGGAGAGAAGAGTGCATTATAGACTGCGAGATTCAGATCAGAGT								853
OY	146	tgcttaaacagtagaagaccgccgagagaactacttggcttggttaccagacagaacaccagggcagc								205
Db	854	TGTTCAACAGTAGAAGAACCCGAAGAAGACTGTAAGTGTGGTACACAGACAAGAACAGGGCAGT								913
OY	206	cctctaatacctcgtgcttactcttgggcacctccaactagggaatctggggctccctgatgcttca								265
Db	914	CTCCATAACCCCTGATCTTACTGGGCGCATCCACTAGGGAATCTGGGGTCCCTGATCTCTTCA								973
OY	266	gtgagagtgagctctgggacagattcactctccacatcacagcatgctgaagtgtaagacg								325
Db	974	CAGGAGTGAGTACTGGGACAGATTCACCTTCACCATCAGCAGTGTGACGGCTGAAGACC								1033
OY	326	tgagcatttatctacgcgcagcatcttaatactttacacgcttcggaagggagacag								385
Db	1034	TGGCAGATTATATTACGACAGACATTTATATTCTTCGGACGTCGCTGGTAGGACACCAAGC								1093
OY	386	tggaataaaaa 396								
Db	1094	TGGAATTTAAA 1104								
<hr/>										
RESULT 3										
PCT-US93-11611-1										
Sequence 1, Application PC/TUS9311611										
GENERAL INFORMATION:										
APPLICANT: CO., Man Sung										
APPLICANT: Landolf, Nicholas F.										
TITLE OF INVENTION: Humanized Antibodies Reactive with CD18										
NUMBER OF SEQUENCES: 11										
CORRESPONDENCE ADDRESS:										
ADDRESSEE: Townsend and Townsend Kourlie and Crew										
STREET: One Market Plaza, Stuart Tower, Suite 2000										
CITY: San Francisco										
STATE: California										
COUNTRY: USA										
ZIP: 94105										
COMPUTER READABLE FORM:										
MEDIUM TYPE: Floppy disk										
COMPUTER: IBM PC compatible										
OPERATING SYSTEM: PC-DOS/MS-DOS										
SOFTWARE: Patent Release #1.0, Version #1.25										
CURRENT APPLICATION DATA:										
APPLICATION NUMBER: PCT/US93/11611										
FILING DATE: 30-NOV-1993										
CLASSIFICATION:										
PRIOR APPLICATION DATA:										
APPLICATION NUMBER: US 07/983,949										
FILING DATE: 01-DEC-1992										
ATTORNEY/AGENT INFORMATION:										
NAME: Smith, William M.										
REGISTRATION NUMBER: 30,223										
REFERENCE/DOCKET NUMBER: 11823-45										
TELECOMMUNICATION INFORMATION:										
TELEPHONE: 415-326-2400										
TELEFAX: 415-326-2422										
INFORMATION FOR SEQ ID NO: 1:										
SEQUENCE CHARACTERISTICS:										
LENGTH: 399 base pairs										
TYPE: nucleic acid										
STRANDEDNESS: single										
TOPOLOGY: linear										
MOLECULE TYPE: cDNA										
FEATURE:										

FILING DATE: 01-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 399 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..399
 PCT-US93-11612-1

Query Match 66.8%; Score 264.6; DB 6; Length 399;
 Best Local Similarity 80.7%; Pred. No. 3.5e-76;
 Matches 322; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

QY 1 atgattcacaggcccggtcttattatgtctgtatggtatctgacactgtg 60
 DB 1 atgattcacaggcccggtcttattatgtctgtatggtatctgacactgtg 60
 QY 61 gacattgtctgacacagcttcacagatccctgtgctgtaagcttaaggagagagccact 120
 DB 61 gacattgtctgacacagcttcacagatccctgtgctgtaagcttaaggagagagccact 120
 QY 121 atgactgcaaaatcccgatcagatctctcaacagctagaaccgagagaaactcttgct 180
 DB 121 atgactgcaaaatcccgatcagatctctcaacagctagaaccgagagaaactcttgct 180
 QY 121 atgacctgcaagctccactcagacgaccttttaaatgtagcaatcamaagaactatttgccc 180
 DB 121 atgacctgcaagctccactcagacgaccttttaaatgtagcaatcamaagaactatttgccc 180
 QY 181 tggtagcagagaagaacagagcagcctccctaaactgtgtactcagcagcagcagcagcagc 240
 DB 181 tggtagcagagaagaacagagcagcctccctaaactgtgtactcagcagcagcagcagcagc 240
 QY 241 gaactctgggtccctgacgcttcagtgagtgagtgagtgagtgagtgagtgagtgagtgag 300
 DB 241 gaactctgggtccctgacgcttcagtgagtgagtgagtgagtgagtgagtgagtgagtgag 300
 QY 301 atcagcagctgctgacgcttcagtgagtgagtgagtgagtgagtgagtgagtgagtgag 360
 DB 301 atcagcagctgctgacgcttcagtgagtgagtgagtgagtgagtgagtgagtgagtgag 360
 QY 358 cttaacagctcggagacagagcagagtgagaaataaa 396
 DB 361 ccgctcacgttcgctgctgggacacacagctgagctgaaa 399

RESULT 9
 US-07-916-098A-34
 Sequence 34, Application US/07916098A
 Patent No. 5871733

GENERAL INFORMATION:
 APPLICANT: BORKLY, LINDA C.
 APPLICANT: CHISHOLM, PATRICIA L.
 APPLICANT: THOMAS, DAVID W.
 APPLICANT: ROSA, MARGARET D.
 APPLICANT: ROSA, JOSEPH J.
 TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
 TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
 STREET: 10 SOUTH WACKER DRIVE
 CITY: CHICAGO
 STATE: ILLINOIS
 COUNTRY: U.S.A.

ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/916,098A
 FILING DATE: July 24, 1992
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/08843
 FILING DATE: No. 5871732ember 27, 1991
 CLASSIFICATION: 424
 APPLICATION NUMBER: 07/618,542
 FILING DATE: No. 5871732ember 27, 1990
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: JOHN J. MC DONNELL
 REGISTRATION NUMBER: 26,949
 REFERENCE/DOCKET NUMBER: 92,310-G
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 715-1000
 TELEFAX: (312) 715-1234
 TELEX: 910/221-5317
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 344 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: misc-feature
 LOCATION: 1
 OTHER INFORMATION: /note= "PMDR1003 insert"
 US-07-916-098A-34

Query Match 62.7%; Score 248.2; DB 3; Length 344;
 Best Local Similarity 84.1%; Pred. No. 6.2e-71;
 Matches 280; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 60 ggaacttggtgacacagcttcacagatccctggtgtaagcttaaggagagggccac 119
 DB 10 ggaacttggtgacacagcttcacagatccctggtgtaagcttaaggagagggccac 119
 QY 120 tatagctgaatccagtcagagcttcagcagcttcagcagcttcagcagcttcagcagcttcag 179
 DB 70 tatagctgaatccagtcagagcttcagcagcttcagcagcttcagcagcttcagcagcttcag 129
 QY 180 ttggtaccagcagaaacagagcagcctccctaaactgtgactatcagtgagcagcagcagc 239
 DB 130 ctggtaccagcagaaacagagcagcctccctaaactgtgactatcagtgagcagcagcagc 189
 QY 240 ggaacttggtgacacagcttcacagatccctggtgtaagcttaaggagagggccac 299
 DB 190 ggaacttggtgacacagcttcacagatccctggtgtaagcttaaggagagggccac 249
 QY 300 catcagcagctcggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 359
 DB 250 catcagcagctcggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 309
 QY 360 ttacagcttcggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 392
 DB 310 tcgacagcttcggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 342

RESULT 10
 US-08-467-420A-50
 Sequence 50, Application US/08467420A


```
? Patent No. 5683892
? GENERAL INFORMATION:
? APPLICANT: Ames, Robert S.
? APPLICANT: Appelbaum, Edward R.
? APPLICANT: Chaiken, Irwin M.
? APPLICANT: Cook, Richard M.
? APPLICANT: Gross, Mitchell S.
? APPLICANT: Holmes, Stephen D.
? APPLICANT: McMillan, Lynette J.
? APPLICANT: Theisen, Timothy W.
? TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
? TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
? NUMBER OF SEQUENCES: 74
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SmithKline Beecham Corp./Corporate
? ADDRESSEE: Intellectual Property
? STREET: P. O. Box 1539-UW2220
? CITY: King of Prussia
? STATE: Pennsylvania
? COUNTRY: USA
? ZIP: 19406-0939
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/467,420A
? FILING DATE:
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/363131
? FILING DATE: 23-DEC-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Sutton, Jeffrey A.
? REGISTRATION NUMBER: 34,028
? REFERENCE/DOCKET NUMBER: P50282
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 610 270-5024
? TELEFAX: 610 270-5090
? INFORMATION FOR SEQ ID NO: 50:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5703 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? US-08-467-420A-50

Query Match 62.4%; Score 247; DB 1; Length 5703;
Best Local Similarity 77.9%; Pred. No. 4.5e-70;
Matches 311; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

QY 1 atgattcacagagccaggtcttatattgtctgctcatgtgatacggaccctgtgg 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1014 ATGGTGTTCAGACACCGAGTTCATTCTGTGCTGCTGATCTCGGCGCCACGG 1073

QY 61 gacattgtctgacacagctctccagatccctgtgctgtgaagcttagagagagggccact 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1074 GATATCGTATGACCCAGCTCTCCAGACTCGCTAGCTGTCTGTGGGAGAGGCCAC 1133

QY 121 attagctgcgaataatcagtcagtcagtcctcaacagtagaacccgagagaactactgtgct 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1134 ATCACTGCGCAAGAGCTCTCAAGTCTGTTAAACAGTGAATCAAAAGACTTACTTGCC 1193

QY 181 tggtaaccagcagaacacagcagcagcctcctaactgctgactactgtggcatccactagg 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1194 TGGTATACGACGAACCCGGGACACCTCTTAAGTTGCTCATTTACGGGGCGCTCAGACTAG 1253

QY 241 gaactcgtgggtccctgctgctcagtcagtcgagtcgagatctggagacagattcaactccacc 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1254 GAATCTGGGTAACCTGACCCGATTCAGTGGCAGCGGGTCTGGAGACAGATTTCACCTCACC 1313
```

```
QY 301 atcagcaagctgcagagcgtgaagagctgagcaggtttattactcagcgaactctataactt 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1314 ATCAGCAAGCTGCGAGGCTGAAGATGTGGCAGTATATCTGTGCAAGATGTTCAATAGTTT 1373

QY 361 --taccagctgcagacagagagcacaagtggaataaa 396
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1374 CCATTCACGCTTCGGGGAGGAGCACCAAGTTGGAGATCAAA 1412

RESULT 11
US-08-470-110A-50
? Sequence 50, Application US/08470110A
? Patent No. 5693323
? GENERAL INFORMATION:
? APPLICANT: Ames, Robert S.
? APPLICANT: Appelbaum, Edward R.
? APPLICANT: Chaiken, Irwin M.
? APPLICANT: Cook, Richard M.
? APPLICANT: Gross, Mitchell S.
? APPLICANT: Holmes, Stephen D.
? APPLICANT: McMillan, Lynette J.
? APPLICANT: Theisen, Timothy W.
? TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
? TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
? NUMBER OF SEQUENCES: 74
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SmithKline Beecham Corp./Corporate
? ADDRESSEE: Intellectual Property
? STREET: P. O. Box 1539-UW2220
? CITY: King of Prussia
? STATE: Pennsylvania
? COUNTRY: USA
? ZIP: 19406-0939
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/470,110A
? FILING DATE:
? CLASSIFICATION: 426
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/363131
? FILING DATE: 23-DEC-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Sutton, Jeffrey A.
? REGISTRATION NUMBER: 34,028
? REFERENCE/DOCKET NUMBER: P50282
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 610 270-5024
? TELEFAX: 610 270-5090
? INFORMATION FOR SEQ ID NO: 50:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5703 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? US-08-470-110A-50

Query Match 62.4%; Score 247; DB 2; Length 5703;
Best Local Similarity 77.9%; Pred. No. 4.5e-70;
Matches 311; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

QY 1 atgattcacagagccaggtcttatattgtctgctcatgtgatacggaccctgtgg 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1014 ATGGTGTTCAGACACCGAGTTCATTCTGTGCTGCTGATCTCGGCGCCACGG 1073

QY 61 gacattgtctgacacagctctccagatccctgtgctgtgaagcttagagagagggccact 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 1074 GATATCGTATGATGACCCAGCTCTCCAGACTGCTAGCTGTCTGTGGGAGAGGCCACC 1133
Qy 121 attagctgaataatccagctagagctgtctccacagtagaacccgaggaactacttgct 180
Db 1134 ATCAACTGCAAGAGCTCTGAGTCTGTTAAACAGGGAATCAAAAGAACTACTTGCGC 1193
Qy 181 tggtaaccagcaaaaccagggagcgcctccaaactctatctactctggtacccactag 240
Db 1194 TGGTATCAGACAAACCCGGGAGCGCTCTTAAGTTGCTATTACGGGCGTCACTAG 1253
Qy 241 gaattggggtccctgcatgcttcagctgagctgagctgagctgagcaatctacc 300
Db 1254 GAATCTGGGGTCTGACCGGATTCAGTGGCAGCGGGCTCGGACAGATTCTACCTCACC 1313
Qy 301 atcagcagctctcagcctcgaagcctgagcttattactgacgcaatctatactt 360
Db 1314 ATCAGCAGCTCTCAGGCTGAAAGATGTGGCAGTATACTGTCAGAAATGTTATGTTT 1373
Qy 361 ---tacagcttcgacaggggacccaagtggaataaa 396
Db 1374 CCATTCACGTTGGGGAGGAGCAAGTTGGAGATCAAA 1412

RESULT 12
US-08-667-769A-50
Sequence 50, Application US/08667769A
Patent No. 5783184

GENERAL INFORMATION:

APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P. O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,769A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17082
FILING DATE: 22-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50503
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024

TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 5703 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-667-769A-50

Query Match 62.4%; Score 247; DB 2; Length 5703;
Best Local Similarity 77.9%; Pred. No. 4,5e-70;
Matches 311; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

Qy 1 atgattacagagccaggtctctatattctgtctgtatggtatctgcaactgtgg 60
Db 1014 ATGGTGTGGCAAGACCCAGGCTTTCATTCTGTGCTGTGATCTCGTGGCTACGGG 1073
Qy 61 gacattgtgctgacagctctccagatccctggtgtgtaagcttgaagagagccact 120
Db 1074 GATATCGTATGATGACCCAGTCTCCAGACTCGCTAGCTGTGCTCTGGGCGAGGGCCACC 1133
Qy 121 attagctgaataatccagctagagctgtctccacagtagaacccgaggaactacttgct 180
Db 1134 ATCAACTGCAAGAGCTCTGAGTCTGTTAAACAGTGAATCAAAAGAACTACTTGCGC 1193
Qy 181 tggtaaccagcaaaaccagggagcgcctccaaactctatctactctggtacccactag 240
Db 1194 TGGTATCAGACAAACCCGGGAGCGCTCTTAAGTTGCTATTACGGGCGTCACTAG 1253
Qy 241 gaattggggtccctgcatgcttcagctgagctgagctgagctgagcaatctacc 300
Db 1254 GAATCTGGGGTCTGACCGGATTCAGTGGCAGCGGGCTCGGACAGATTCTACCTCACC 1313
Qy 301 atcagcagctctcagcctcgaagcctgagcttattactgacgcaatctatactt 360
Db 1314 ATCAGCAGCTCTCAGGCTGAAAGATGTGGCAGTATACTGTCAGAAATGTTATGTTT 1373
Qy 361 ---tacagcttcgacaggggacccaagtggaataaa 396
Db 1374 CCATTCACGTTGGGGAGGAGCAAGTTGGAGATCAAA 1412

RESULT 13
US-08-940-371-50
Sequence 50, Application US/08940371
Patent No. 5851525
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P. O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,371
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,110
; FILING DATE:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sulton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270-5024
; TELEFAX: 610 270-5090
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; US-08-940-371-50

Query Match          62.4%; Score 247; DB 3; Length 5703;
Best Local Similarity 77.9%; Pred. No. 4.5e-70;
Matches 311; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

QY 1 atgattcacaagccaggtctctatatatgtcgtctatggtgagatcgacctgtgg 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1014 ATGTTGTTCAGACCCAGGCTCTTCTCTGTGCTCTGATCTGTGCTTACGGG 1073

QY 61 gacattgtctgacacagctccagattccctgtgctgtaagcttagagagagggccact 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1074 GATATGCTGATGACCCAGCTCCAGACTCGTACTGTGCTGTCTGTGGCGAGAGGGCCACC 1133

QY 121 attagctgcaaatccagtcagtcagtcctcaacagtagaacccgagagaactacttggct 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1134 ATCAACTGCAAGAGCTCTCAGAGCTGTAAACAGTGAATCAAAAGAACTACTTGGCC 1193

QY 181 tggtaaccagagaacacagggcagcctccctaaactgtgactctactggtggaactcagg 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1194 TGGTATCAGACAGAAACCCGGGACCTCTTAAGTGTCTCATTTACGGGGGCTGCACCTAGG 1253

QY 241 gaactctgggtccctgatacgtcttcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1254 GAATCTGGGGTACTGACCATTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 1313

QY 301 atcagcagctcgcagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtc 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1314 ATCAGCAGCTCGCAGGCTGAAGATGTGCGAGTACTACTGTCAGAAATGTTCAATAGTTT 1373

QY 361 ---tacacgttcggagacaggggacccaaggtggaataaaa 396
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1374 CCATTACGTTGGCGGAGGACCAAGTTGAGATCAAA 1412

RESULT 14
PCT-US95-17082A-50
; Sequence 50, Application PC/TUS9517082A
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theissen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
```

```

; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-0W2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17082A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER:
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sulton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-17082A-50

Query Match          62.4%; Score 247; DB 6; Length 5703;
Best Local Similarity 77.9%; Pred. No. 4.5e-70;
Matches 311; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

QY 1 atgattcacaagccaggtctctatatatgtcgtctatggtgagatcgacctgtgg 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1014 ATGTTGTTCAGACCCAGGCTCTTCTCTGTGCTCTGATCTGTGCTTACGGG 1073

QY 61 gacattgtctgacacagctccagattccctgtgctgtaagcttagagagagggccact 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1074 GATATGCTGATGACCCAGCTCCAGACTCGTACTGTGCTGTCTGTGGCGAGAGGGCCACC 1133

QY 121 attagctgcaaatccagtcagtcagtcctcaacagtagaacccgagagaactacttggct 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1134 ATCAACTGCAAGAGCTCTCAGAGCTGTAAACAGTGAATCAAAAGAACTACTTGGCC 1193

QY 181 tggtaaccagagaacacagggcagcctccctaaactgtgactctactggtggaactcagg 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1194 TGGTATCAGACAGAAACCCGGGACCTCTTAAGTGTCTCATTTACGGGGGCTGCACCTAGG 1253

QY 241 gaactctgggtccctgatacgtcttcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1254 GAATCTGGGGTACTGACCATTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 1313

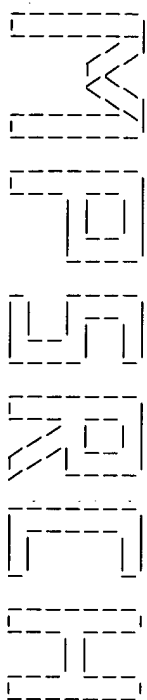
QY 301 atcagcagctcgcagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtc 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1314 ATCAGCAGCTCGCAGGCTGAAGATGTGCGAGTACTACTGTCAGAAATGTTCAATAGTTT 1373

QY 361 ---tacacgttcggagacaggggacccaaggtggaataaaa 396
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


Sun Aug 27 09:11:16 2000

us-09-249-011-7.rni

Page 11



Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (C) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Run on: Mon Aug 7 19:03:11 2000; Maspar time 12.30 Seconds
Tabular output not generated. 506.103 Million cell updates/sec

Title: >US-09-249-011-8
Description: (1-132) from US09249011.pep
Perfect Score: 943
Sequence: 1 MDSQAVLLILLWVSGTGG.....YCGSYNLTFGGKTVEIK 132

Scoring table:
PAM 150
Gap 11

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r64
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 41.834; Variance 96.432; scale 0.434

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	819	86.9	133	2	PS0023	Ig kappa chain precur 7.45e-121
2	777	82.4	120	2	G33932	Ig kappa chain precur 2.48e-113
3	776	82.3	134	2	S49531	anti-sm antibody VL c 3.74e-113
4	764	81.0	134	1	K4H017	Ig kappa chain precur 5.23e-111
5	759	80.5	133	1	K4H0J1	Ig kappa chain precur 4.09e-110
6	745	79.0	134	2	S21917	Ig kappa chain V regi 1.29e-107
7	744	78.9	138	2	A53261	Ig kappa chain precur 1.95e-107
8	744	78.9	145	2	PL0014	Ig kappa chain precur 1.95e-107
9	743	78.8	132	2	S46373	Ig kappa chain V-J re 2.94e-107
10	743	78.8	134	2	PC1214	Ig kappa chain precur 2.94e-107
11	740	78.5	129	2	S40347	Ig kappa chain - huma 1.01e-106
12	734	77.8	240	2	S06084	Ig kappa chain precur 1.18e-105
13	725	76.9	135	2	S38807	Ig kappa chain V-J re 4.76e-104
14	715	75.8	121	1	K4HU	Ig kappa chain precur 2.87e-102
15	713	75.6	138	2	S26040	Ig kappa chain precur 6.52e-102
16	709	75.2	124	2	S40364	Ig kappa chain - huma 3.36e-101
17	700	74.2	136	2	A49137	Ig kappa chain precur 1.34e-99
18	694	73.6	113	2	PT0407	Ig kappa chain V regi 1.56e-98
19	688	73.0	120	2	S51147	antibody light chain 1.82e-97
20	683	72.4	114	1	K4H0J1	Ig kappa chain V-J re 1.40e-96
21	682	72.3	112	2	S43103	Ig kappa chain V-J re 2.11e-96
22	680	72.1	129	2	S40329	Ig kappa chain V-J re 4.79e-96
23	679	72.0	113	2	S34002	Ig kappa chain V regi 7.20e-96

24	675	71.6	113	2	PT0408	Ig light chain V regi 3.69e-95
25	669	70.9	112	2	PL0265	Ig kappa chain V regi 4.28e-94
26	666	70.6	113	2	S30520	Ig kappa chain V regi 1.46e-93
27	657	69.7	103	2	PH1047	Ig light chain V regi 5.73e-92
28	655	69.5	112	2	S41393	Ig kappa chain V regi 1.29e-91
29	650	68.9	103	2	PH1052	Ig light chain V regi 9.94e-91
30	647	68.6	114	2	S44119	Ig kappa chain V-J re 3.37e-90
31	642	68.1	111	2	S03304	Ig kappa chain V regi 2.59e-89
32	642	68.1	113	2	S34003	Ig kappa chain V regi 2.59e-89
33	642	68.1	114	2	S44116	Ig kappa chain V-J re 2.59e-89
34	641	68.0	104	2	PH1101	Ig light chain V-J re 3.89e-89
35	639	67.8	104	2	PH1102	Ig light chain V regi 8.77e-89
36	638	67.7	104	2	PH1104	Ig light chain V regi 1.32e-88
37	637	67.6	103	2	PH1051	Ig light chain V regi 1.98e-88
38	633	67.1	101	2	PH1046	Ig light chain V regi 1.01e-87
39	633	67.1	113	2	S30523	Ig kappa chain V regi 1.01e-87
40	632	67.0	103	2	PH1050	Ig light chain V regi 1.51e-87
41	632	67.0	131	2	S40372	Ig kappa chain V-J re 1.51e-87
42	627	66.5	104	2	PH1103	Ig light chain V-J re 1.74e-86
43	626	66.4	136	2	S40357	Ig kappa chain V-J re 5.88e-86
44	623	66.1	113	2	PL0263	Ig kappa chain V regi 1.33e-85
45	621	65.9	126	2	S40339	Ig kappa chain - huma

ALIGNMENTS

RESULT 1
ENTRY PS0023 #type complete
TITLE Ig kappa chain precursor V region (6A4) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 13-Sep-1998

ACCESSIONS
REFERENCE
#authors Margaret, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.;
#journal Gene (1988) 74:335-345
#title Cloning and characterization of cDNAs coding for the heavy and light chains of a monoclonal antibody specific for Pseudomonas aeruginosa outer membrane protein I.
#cross-references M01D:89232725
#accession PS0023
##molecule_type mRNA
##residues 1-133 ##label VAR
##experimental_source strain BALB/c
##note the amino-terminal four residues of the mature protein were directly sequenced

COMMENT This chain was obtained from a monoclonal antibody against Pseudomonas aeruginosa lipoprotein I.
CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology
KEYWORDS #heterotrimer; Immunoglobulin
FEATURE
1-20 #domain signal sequence #status predicted #label SIG
21-133 #product Ig kappa chain V region 6A4 #status experimental #label IGV

SUMMARY #length 133 #molecular-weight 14513 #checksum 1662

Query Match 86.9%; Score 819; DB 2; Length 133;
Best Local Similarity 86.4%; Pred. No. 7.45e-121;
Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
Db 1 MDSQAVLLILLWVSGTGGCGIVLTPSDSLAVSGEATRTSCSSOSLSLRRENTA 60
Qy 1 MDSQAVLLILLWVSGTGGCGIVLTPSDSLAVSGEATRTSCSSOSLSLRRENTA 60
Db 61 WYQKPGSPKLLIYMASTRSGVDPDRSGSGSGDFLITSSVOAEDLAVYYCKOSYNL 120
Qy 61 WYQKPGSPKLLIYMASTRSGVDPDRSGSGSGDFLITSSVOAEDLAVYYCTQSYNL 120
Db 121 RTFGGKTVEIK 132
Qy 121 RTFGGKTVEIK 132
Qy 121 YTFGGTVEIK 132

```

RESULT      4
ENTRY      K4HU17      #type complete
TITLE      Ig kappa chain precursor V-IV region (B17) - human
ORGANISM   Homo sapiens #common_name man
DATE       30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
ACCESSIONS A01905
REFERENCE   A01905
AUTHORS     Marsh, P.; Mills, F.; Gould, H.
JOURNAL     Nucleic Acids Res. (1985) 13:6531-6544
TITLE       Detection of a unique human V kappa avy germline gene by a
           cloned cDNA probe.
#cross-references MIMD:86041854
#accession      A01905
#molecule_type mRNA
#residues       1-134 ##label MAR
#note           the sequence was determined from the differentiated gene
#note           the authors translated the codon TGC for residue 76 as
#note           Trp
COMPLEX
An immunoglobulin heterotrimer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
#superfamily immunoglobulin V region; immunoglobulin homology
heterotrimer; immunoglobulin
CLASSIFICATION
KEYWORDS     #domain signal sequence #status predicted #label SIG\
FEATURE      #product Ig kappa chain V-IV region (B17) #status
1-20         predicted #label MAR\
21-134       #region framework 1\
           #region complementarity-determining 1\
44-60        #region framework 2\
61-75        #region complementarity-determining 2\
76-82        #region framework 3\
83-114       #region complementarity-determining 3\
115-121      #region framework 4\
122-134      #disulfide_bonds #status predicted
43-114       #length 134 #molecular_weight 14863 #checksum 2111
SUMMARY
Query Match      81.0%; Score 764; DB 1; Length 134;
Best Local Similarity 84.2%; Pred. No. 5,23e-11;
Matches 112; Conservative 7; Mismatches 13; Indels 1; Gaps 1;
Db 1 MYLOTQVFLSLMISAGADYMTQSPDLSAVSGEARTITCKSSQSLTSSDNKAYLA 60
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 1 MDSQAQVLLILLVMSQTCGDYLTQSPDLSAVSGEARTITCKSSQSLNRTRENTLA 60
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 WYQKPPQPKRLIYCASTRESGVPRFGSSGSGDFLTITSLQAEVAVYYCCQYYNL 120
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 61 WYQKPPQPKRLIYNASTRESGVPRFGSSGSGDFLTITSLQAEVAVYYCTQSYNL 120
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 121 PWFPGGCTKVEIK 133
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 121 -YTFGGCTKVEIK 132
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT      5
ENTRY      K4HUJ1      #type complete
TITLE      Ig kappa chain precursor V-IV region (J1) - human
ORGANISM   Homo sapiens #common_name man
DATE       30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
ACCESSIONS A01904
REFERENCE   A03589
AUTHORS     Klobenz, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.;
           Pohlenz, H.D.; Zachau, H.G.
JOURNAL     Nucleic Acids Res. (1985) 13:6515-6529
TITLE       Subgroup IV of human immunoglobulin K light chains is encoded
           by a single germline gene.
#cross-references MIMD:86041853

```



```

#accession      A01904
#molecule_type DNA
#residues      1-133 ##label KLO
#cross-references GB:200022; GB:X51570; NID:g33156; PIDN:CAA77317.1;
                    PID:g296654
#note          the sequence was determined from the differentiated gene
GENETICS
#gene          GDB:IGKV
#cross-references GDB:119341; OMIM:146980
#map_position  2p12-2p12
#intons
COMPLEX
An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
#superfamily  immunoglobulin V region; immunoglobulin homology
heterotetramer; immunoglobulin V
CLASSIFICATION
KEYWORDS
FEATURE
1-20
21-133
21-43
44-60
61-75
76-82
83-114
115-122
123-133
43-114
#length 133 #molecular-weight 14632 #checksum 1869
SUMMARY
Query Match      80.5%; Score 759; DB 1; Length 133;
Best Local Similarity 82.7%; Pred. No. 4,09e-110;
Matches 110; Conservative 8; Mismatches 13; Indels 2; Gaps 2;

Db 1 MYLQVVFSLIMISGAGDIYMTGSPDSLAVSLGERRATINCKSSGVLYSSNNKYLA 60
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 1 MDSQAVLLILLWAGTGGDYLITGSPDSLAVSLGERATISCKSSGSLNSTRRENYLA 60
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 61 WYQKRGQPPKLLIYVASTRESGVPRFSSGSGTPTLTITSSLQADVAIVYCCQ-YDT 119
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 WYQKRGQPPKLLIYVASTRESGVPRFSSGSGTPTLTITSSLQADVAIVYCCQSYNL 120
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 120 IPTFGGGRFVEIK 132
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 121 Y-TFGGGRFVEIK 132
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 6
ENTRY      S21917 #type complete
TITLE      Ig kappa chain V region precursor - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       20-Feb-1995 #sequence_revision 20-Feb-1995 #text-change
                23-Jul-1999
ACCESSIONS S21917
REFERENCE   S21916
#authors    Mierau, R.; Gause, A.; Kuennpers, R.; Michels, M.; Mageed,
#submission R.A.; Jefferis, R.; Genth, E.
#description submitted to the EMBL Data Library, July 1991
                A human monoclonal IgA rheumatoid factor using the VK(IV)
                light chain gene.
#accession  S21917
#status     preliminary
#molecule_type DNA
#residues   1-134 ##label MIE
#cross-references EMBL:X61125; NID:g33288; PIDN:CAA43437.1; PID:g33289
CLASSIFICATION
KEYWORDS    #superfamily immunoglobulin V region; immunoglobulin homology
                heterotetramer; immunoglobulin
SUMMARY     #length 134 #molecular-weight 14796 #checksum 3898

Query Match      79.0%; Score 745; DB 2; Length 134;

```

[illegible]

##residues	1-145	##label	CHE
##experimental	source cell line F6-3		
COMMENT	This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine response.		
CLASSIFICATION	#superfamily Immunoglobulin V region; immunoglobulin homology		
KEYWORDS	heterotetramer; Immunoglobulin		
FEATURE			

```

1-20    #oomin signal sequence #status predicted #label size
21-134 #product if heavy chain v region (4C11) #status
        predicted #label MAR\
44-60   #region complementarity-determining 1\
76-82   #region complementarity-determining 2\
115-123 #region complementarity-determining 3\
135-145 #domain constant region (I4gment) #status predicted

```

```
SUMMARY      #length 145  #checksum 6078
```

Query Match	78.9%;	Score 744;	DB 2;	Length 145;
Best Local Similarity	78.4%;	Pred. No. 1.95e-107;		
Matches	105;	Conservative	15;	Mismatches 11; Indels 3; Gaps 2;

Dd 1 MDSQAQVLMELLMLWSSGTCGGDIWMSQSPPSLAVSNGEKVTMSCSQSSQLLYNSNQKNFLA 60
|||||:|||||||::||| |||||: |:| | ||||| : |:| |
Qy 1 MDSQAQVLILLMLWSSGTCGGDIYLTQSPSLAVSLGERATISCKSSQSSLNRPRENTYLA 60

```

Db      61 WYQKPGQSPKLLIYNASTREGVPPDRRTGSGSTDTLLTSSVAEDLNAVYCCQYDSY 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 WYQKPGQSPKLLIYNASTREGVPPDRRTGSGSTDTLLTSSVAEDLNAVYCCQY--SY 118

```

```

Db      121 PL-TFGSGTKLEMK 133
      | | | | | | | |
Qy      119 NLYTFGGGKTVEIK 132

```

RESULT	9
ENTRY	S46373
TITLE	Ig kappa chain V-J region (T24-9) - human (fragment)
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 22-Jul-1995

ACCESSIONS	REFERENCE
S46373; S38647	Bensimon, C.; Chastagner, P.; Zouali, M.
S46369	Embo J. (1994) 13:2951-2962
#authors	Human lupus anti-DNA autoantibodies undergo essentially
#journal	primary V(Chi) gene rearrangements.
#title	#cross-references MIMD:94313975

```

#residues      1-132 #label BEN
#cross-references EMBL:Z27117; NID:9415963; PIDN:CAAB1698.1;
#superfamily immunoglobulin V region; immunoglobulin
heterotetramer; immunoglobulin
#length 132 #checksum 1087

```

Query Match	78.8%;	Score 743;	DB 2;	Length 132;
Best Local Similarity	79.2%;	Pred. No. 2.94e-107;		
Matches	103;	Conservative	14;	Mismatches 12;
			Indels	1;
			Gaps	1;

```
Db      2 QTOVFISLLMLISGAGDVMFOSPDSLAVSLGERATINCKSSQSVLSSNNKNYLAWQ 61
         |:::| |:::| : |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Qy     4 QAQVILLIILMWSGTCGDIVLPSPDSLAVSLGERATISCSSQSLSNSTRREYLAWQ 63
```

```
D6 QKPGPPKKLLIHWASSRESGVLDRFSGGSGTPTLTITSSIQTEDEVAVYCHQYYSPFT 121
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
07   64 QKPGRPKLLIWASRRESGVDRFSSGGSGTDPTLTISSLQAEDVAVVYTQTSYN-LYT 122
```

Db 122 FGPGTKVDIK 131
1111111111
QY 123 FGGTKVEIK 132

RESULT	ENTRY	TITLE	ORGANISM	DATE	ACCESSIONS
10	PC1214	#type fragment Ig kappa chain precursor V region (mab H8) - mouse (fragment)	#common_name house mouse	#30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Jul-1999	PC1214

REFERENCE	#authors	#journal	#title
PC1213	Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim, J.; Han, M.H.	Gene (1992) 121:331-335	Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody specific for pre-S antigen of hepatitis B virus.

```
#accession    PC1214 |
```

```
##residues      1-134 ##label HON
##cross-references|GB:M58042; NID:g196749; PIDN:AAA38777.1; PID:g196750
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
```

```

FEATURE
1-20      #domain signal sequence #status predicted #label SIG
21-134    #product Ig light chain V region #status predicted

```

SUMMARY	#length	134	#checksum	4185
Query Match		78.8%	Score 743;	DB 2; Length 134;

Matches 105; Conservative 13; Mismatches 14; Indels 1; Gaps 1

Db 1 MDSGAQVLMILLWYSGTCGIVMSGSPSSLAVSGEYTMCKSSQSLYSSIQNYLA 60

D6
D7

61 MYOORPGSPKLLIYWASTREGVDPDRFTGSGSETDTLLISNKAEDLAVYYCOQRYNY 120
|||||
61 MYOORPGSPKLLIYWASTREGVPDRFSGSGSGETDTLLISLAQADVAAYCTOSYNL 120

101 DGGGCGGGRWTW 123

Qy	121	-YTFGGTKRVEIK	132
RESULT	11		
ENTRY	S40347	#type complete	
TITLE	Ig kappa chain - human		

```

DATE          00-Feb-1994 #sequence_revision 20 May 1993 #rev=1
ACCESSIONS
REFERENCE     S40347 |
               S40312 |
#authors      Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal      Eur. J. Immunol. (1993) 23:3248-3271
#title        Expressed human immunoglobulin chi genes and their

```

```
#cross-references MUID: 94080891
#accession      S40347 |
#status          preliminary; translation not shown
```

#Residues	1-129	#label	RLE
#Cross-references	EMBL:X72457;	NID:g441382;	PIDN:CAA51125.1
	PID:g441383		

KEYWORDS heterotetramer; immunoglobulin

SUMMARY #length 129 #molecular-weight 14370 #checksum 6948

	Best Local Similarity	Pred. No. 1.01e-106;	Matches 105; Conservative	Mismatches 13; Indels 1; Gaps 1
db	1	OTQVSIILMIISGAGDIIVTQSPDSLTSLVSLGERATINCKSSQSVLYSFNNKNYLA	60	

```

Oy      4  QAOVILLLILMWASGTGCDIVLTQSPDLSAVSLGERATISCKSSQSLNSTRRENYLAWYQ 63
Db      61  QKPGQPOLLITWASTRESGVPPRFGSGSGGDTFTLTINSLQAEADVAVYYCCQYKTPLT 120
Oy      64  QKPGQPPLLITWASTRESGVPPDRFGSGSGGDTFTLTISLQAEADVAVYYCTQSYNL-YT 122
Db      121  FGGGTGEVEI 129
Oy      123  FGGGTKEI 131

RESULT 12
ENTRY      12
TITLE      Ig kappa chain precursor - rat
ORGANISM   Rattus norvegicus
DATE       28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
10-Sep-1997

ACCESSIONS
REFERENCE   #authors
            #journal
            #title
#cross-references MUID:90016888
#accession S06084
#molecule_type mRNA
#residues 1-240 ##label CRO
KEYWORDS   #cross-references EMBL:X16129; NID:g56457; PID:g56458
FEATURES   heterotrimer; immunoglobulin
            #domain signal sequence #status predicted #label SIG\
            #product Ig kappa chain #status predicted #label MAR
            #length 240 #molecular_weight 26397 #checksum 8622
SUMMARY    Query Match 77.8%; Score 734; DB 2; Length 240;
            Best Local Similarity 75.9%; Pred. No. 1,18e-105;
            Matches 101; Conservative 17; Mismatches 14; Indels 1; Gaps 1;

Db      1  MESQTQVLMSLLMTISGTCGDEPYMTQSPSSLAVSAGETVITNCKSSQSLFYSGNOKNYLA 60
Oy      1  MDSQAOVILLLILMWASGTGCDIVLTQSPDLSAVSLGERATISCKSSQSLNSTRRENYLA 60
Db      61  WYQQRPGSGPKLLITWASTRSGVPPRFGSGGDTFTLTISVQAEADLAIYCCQYET 120
Oy      61  WYQQRPGGPPLLITWASTRESGVPPRFGSGSGGDTFTLTISLQAEADVAVYYCTQSYNL 120
Db      121  PYTFGAGTKLEIK 133
Oy      121  YTFGGTKVEIK 132

RESULT 13
ENTRY      13
TITLE      Ig light chain V-J region
ORGANISM   Mus musculus
DATE       19-May-1994 #sequence_revision 26-May-1995 #text_change
16-Aug-1996

ACCESSIONS
REFERENCE   #authors
            #journal
            #title
#cross-references MUID:92267566
#accession S38807
#status preliminary
#molecule_type mRNA
#residues 1-135 ##label SEQ
KEYWORDS   #cross-references EMBL:X59816
FEATURES   the authors translated the codon GGC for residue 1 as
            Ala and TGT for residue 21 as TTP
            #superfamily immunoglobulin V region; immunoglobulin homology

```

[illegible]

QY 61 WYQKPGQPKLLIYWASTRESGVDPDRFSGSGGTDTFTLTSSLAQEDVAVYYCTQSYN 119

RESULT 15
ENTRY S26040 #type fragment
TITLE Ig kappa chain precursor - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 23-Jul-1999
S26040: S78098

ACCESSIONS
REFERENCE S09216
#authors Okamoto, M.; Honjo, T.
#journal Nucleic Acids Res. (1990) 18:1895
#title Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autoantibody produced by a hybridoma from NZB mouse.
#cross-references MUID:90245589
#accession S26040
#molecule_type DNA
#residues 1-138 #label OKA
#cross-references EMBL:X51742
#note the authors translated the codon AGC for residue 107 as Thr and AGT for residue 108 as Thr

REFERENCE
#authors Okamoto, M.
#submission submitted to the EMBL Data Library, February 1990
#accession S78098
#molecule_type DNA
#residues 1-87, 'W', 89-138 #label OKW
#cross-references EMBL:X51742; NID:952697; PIDN:CAA36032.1; PID:952698

GENETICS
#introns 22/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-25 #domain signal sequence #status predicted #label SIG
26-138 #product Ig kappa chain (fragment) #status predicted
#label MAT

SUMMARY
#length 138 #checksum 910

Query Match 75.68; Score 713; DB 2; Length 138;
Best Local Similarity 75.28; Pred. No. 6.52e-102;
Matches 103; Conservative 18; Mismatches 11; Indels 5; Gaps 1;

Db 1 MDSQAOVLMLLLWVSGEKKFSTGCDIVMSGSSSLTVSGEYTMNCKSSQSILYSNNQ 60
QY 1 MDSQAOVLMLLLWVSG-----TCGDLVLTQSPDSLAVSLGERATISCKSSQSILNSRTR 55
Db 61 KNYLAWYQQRPGQPKLLIYWASTRESGVDPDRFSGSGGTDTFTLTSSVKAEDLAVYFCQ 120
QY 56 ENYLAWYQQRPGQPKLLIYWASTRESGVDPDRFSGSGGTDTFTLTSSLAQEDVAVYYCT 115
Db 121 QYTSFLTFGAGTKLEK 137
QY 116 QSYNLTFTFGGQTKVEIK 132

Search completed: Mon Aug 7 19:03:26 2000
Job time : 15 secs.

(TM)

Distribution rights by Oxford Molecular Ltd

generated

1 MDSQAQVLLLLWVSGTCG.....YCTQSYNLYTFEGQGTKEIK 132

2AM 1.50

35661 seqs, 30989116 residues

Listing first 45 summaries

1:swissprot

mean 41.983; variance 65.812; scale 0.638

ved by analysis of the total score distribution

SUMMARIES

5.2 111 1 KV30_MOUSE IG KAPPA CHAIN V-III R 2.20e-101

45	491	52.1	111	1	KV3A_MOUSE	IG KAPPA CHAIN V-III R	9.83e-94
----	-----	------	-----	---	------------	------------------------	----------

ALIGNMENTS

Sequence 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 84.0%; Score 792; DB 1; Length 134;
 Best Local Similarity 85.0%; Pred. No. 8.73e-172;
 Matches 113; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

DB 1 KYLQGVFISLLWISGAGDIWMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLA 60
 1 MDSQAOVLLILLWISGAGDIWMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLA 60
 QY 1 KYLQGVFISLLWISGAGDIWMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLA 60
 DB 61 WYQKRGQPKLLIYWASTRESGVDPDRFGSGSGTDFTLTISLSLAEDVAVYCTQSYNL 120
 QY 61 WYQKRGQPKLLIYWASTRESGVDPDRFGSGSGTDFTLTISLSLAEDVAVYCTQSYNL 120
 DB 121 PWTFGGTRVEIK 133
 QY 121 -YTFGGTRVEIK 132

RESULT 2
 ID KVA8_HUMAN STANDARD; PRT; 133 AA.

AC P06313;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-IV REGION JI PRECURSOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86041853.
 RA Klobbeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
 RA Zachau H.G.;
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
 RT single germline gene."
 RL Nucleic Acids Res. 13:6515-6529(1985).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; 200022; CAA77317.1; -
 DR PIR; A01904; KAHUT1.
 DR HSSP; P01789; 2MCP.
 DR PFAM; PF00047; 1g; 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 1 133 IG KAPPA CHAIN V-IV REGION JI.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 123 132 FRAMEWORK 4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 121 121
 SQ SEQUENCE 133 AA; 14632 MM; 5FB3953066744AF4 CRC64;

Query Match 80.5%; Score 759; DB 1; Length 133;
 Best Local Similarity 82.7%; Pred. No. 4.05e-163;
 Matches 110; Conservative 8; Mismatches 13; Indels 2; Gaps 2;

DB 1 WYLQGVFISLLWISGAGDIWMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLA 60
 1 MDSQAOVLLILLWISGAGDIWMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLA 60
 QY 1 WYQKRGQPKLLIYWASTRESGVDPDRFGSGSGTDFTLTISLSLAEDVAVYCTQSYNL 119
 DB 61 WYQKRGQPKLLIYWASTRESGVDPDRFGSGSGTDFTLTISLSLAEDVAVYCTQSYNL 119

QY 61 WYQKRGQPKLLIYWASTRESGVDPDRFGSGSGTDFTLTISLSLAEDVAVYCTQSYNL 120

DB 120 IPTFGGTRVEIK 132

QY 121 Y-TFGGTRVEIK 132

RESULT 3
 ID KVA0_HUMAN STANDARD; PRT; 121 AA.

AC P06312;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-IV REGION PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86041853.
 RA Klobbeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
 RA Zachau H.G.;
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
 RT single germline gene."
 RL Nucleic Acids Res. 13:6515-6529(1985).
 CC -1 MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; 200023; CAA77318.1; -
 DR PIR; A01902; KAHU.
 DR HSSP; P01789; 2MCP.
 DR PFAM; PF00047; 1g; 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 1 121 IG KAPPA CHAIN V-IV REGION.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 121 FRAMEWORK 4.
 FT DISULFID 43 114 COMPLEMENTARITY-DETERMINING 3.
 FT NON_TER 121 121 BY SIMILARITY.
 SQ SEQUENCE 121 AA; 13380 MM; 9586AD4180D3974 CRC64;

Query Match 75.8%; Score 715; DB 1; Length 121;
 Best Local Similarity 84.0%; Pred. No. 1.35e-151;
 Matches 100; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

DB 1 WYLQGVFISLLWISGAGDIWMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLA 60
 1 MDSQAOVLLILLWISGAGDIWMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLA 60
 QY 1 MDSQAOVLLILLWISGAGDIWMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLA 60
 DB 61 WYQKRGQPKLLIYWASTRESGVDPDRFGSGSGTDFTLTISLSLAEDVAVYCTQSYNL 119
 QY 61 WYQKRGQPKLLIYWASTRESGVDPDRFGSGSGTDFTLTISLSLAEDVAVYCTQSYNL 119

RESULT 4
 ID KVA4_HUMAN STANDARD; PRT; 114 AA.

AC P01625;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1986 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-IV REGION LEN.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 76004342.
 RA Schneider M., Hilschmann N.;
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of
 RT subgroup IV of the kappa type (Bence-Jones protein Len.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
 RN [2]
 RP REVISION TO 9.
 RA Solomon A.;
 RL Submitted (Aug-1996) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01903; KAHULN.
 DR HSSP: P01789; 2MCP.
 DR PRAM: PF00047; 1g; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 41 55 FRAMEWORK 2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 63 94 FRAMEWORK 3.
 FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 113 FRAMEWORK 4.
 FT DISULFID 23 94 BY SIMILARITY.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;
 Query Match 72.7%; Score 686; DB 1; Length 114;
 Best Local Similarity 86.7%; Pred. No. 5.04e-144;
 Matches 98; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
 Db 1 DIWTFSPDCLAVSLGERATINCKSSOSVLYSSNSKNTLANTYQKPGCPKLLIYMASTR 60
 YQ 21 DIVLTPSPDLSAVSLGERATISCKSSOSLNSRTRENTLAVYQKPGCPKLLIYMASTR 80
 Db 61 ESVGDPDFSGSGSCTDFTLTSSLSQAEVDVANYQOQVSTYRSGCGKLEIK 113
 YQ 81 ESVGDPDFSGSGSCTDFTLTSSLSQAEVDVANYQOQVSTYRSGCGKLEIK 132
 RESULT 5
 ID KY3F HUMAN STANDARD; PRT; 133 AA.
 AC P06310;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 RA Klobbeck H.G., Meindl A., Combario G., Solomon A., Zachau H.G.;
 RT "Human Immunoglobulin kappa light chain genes of subgroups II and
 RT III".
 RL Nucleic Acids Res. 13:6499-6513(1985).
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: Z00020; CA77315.1; -.
 DR PIR: A01890; K2HURP.
 DR PRAM: PF00047; 1g; 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 60 74 FRAMEWORK 2.
 FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 82 113 FRAMEWORK 3.
 FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 123 132 FRAMEWORK 4.
 FT DISULFID 43 113 BY SIMILARITY.
 FT NON_TER 133 133
 SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;
 Query Match 64.9%; Score 612; DB 1; Length 133;
 Best Local Similarity 64.7%; Pred. No. 8.49e-125;
 Matches 86; Conservative 23; Mismatches 22; Indels 2; Gaps 2;
 Db 1 MRPLPAQLGLIMLVPPSSGDVYWTQSPSLPYTLGAPASISCRSSOSLYSDG-NTYLN 59
 YQ 1 MDSQAQVLLILLMLVWSTCGDVLQSPDSLAVSLGERATISCKSSOSLNSRTRENTYLA 60
 Db 60 WFOQRPGQSPRRLLYKYSNDSGYDPDFSGSGSCTDFTLTISRVEADVGYIYMGSTHW 119
 YQ 61 WYQKPGCPKLLIYMASTRSGVDPDFSGSGSCTDFTLTSSLSQAEVDVANYCTOSYNL 120
 Db 120 SMFPGGKVEIK 132
 YQ 121 -YTFGGGKVEIK 132
 RESULT 6
 ID KY3F MOUSE STANDARD; PRT; 132 AA.
 AC P01658;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION MOPC 321 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE OF 1-37.
 RX MEDLINE: 78235887.
 RA Burstein Y., Schechter I.;
 RT "Primary structures of N-terminal extra peptide segments linked to
 RT the variable and constant regions of immunoglobulin light chain
 RT precursors: implications on the organization and controlled
 RT expression of immunoglobulin genes.";
 RL Biochemistry 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-132.
 RX MEDLINE: 73140224.
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse Immunoglobulin chains. Partial amino acid sequence of a kappa
 RT chain.";
 RL Biochemistry 12:749-759(1973).
 CC -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
 CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
 CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
 CC RESIDUES.
 DR PIR: A01933; KVM32.
 DR PRAM: PF00047; 1g; 1.
 KW Immunoglobulin V region; Bence-Jones protein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 59 73 FRAMEWORK 2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 81 112 FRAMEWORK 3.
 FT DOMAIN 113 121 FRAMEWORK 4.
 FT DOMAIN 122 131 FRAMEWORK 4.
 FT DISULFID 43 112 BY SIMILARITY.

FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BA773FBE9 CRC64;

Query Match 64.2%; Score 605; DB 1; Length 132;
Best Local Similarity 59.4%; Pred. No. 5,49e-123;
Matches 79; Conservative 33; Mismatches 18; Indels 3; Gaps 3;

DB 1 METDPLLWLLWLPSTGDIYLTQSPASLAVSLQARATISCRASKV-NTYG-NSFMZ 58
1 MSQAQVLLILLWVSGTGDIVLTQSPDLSLGERATISCKSSQSLNSRRENTYA 60
QY 59 WYZAKGZPKLLIYRASLZSGIPARFSGSGSRBFTLTIBPVZABDVATFCZSEBZ 118
61 WYQKRGQPKLLIYWASTRESGVDPDRFSGSGGTDFLTLSLQAEADVAVYYCTQSY- 119
DB 119 PWTFGGTVEIK 131
QY 120 LYTFGGTVEIK 132

RESULT 7
ID KV3M_HUMAN STANDARD; PRT; 129 AA.

AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION HIC PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 88171307.
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RT J. Exp. Med. 167:840-852(1988).
RL -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.

CC PIR; P10022; K3HUH1.
DR HSSP; P01789; 2MCP.
DR PFAM; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.

FT CHAIN 1 20
FT DOMAIN 21 129 IG KAPPA CHAIN V-II REGION HIC.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B874D6 CRC64;

Query Match 63.5%; Score 599; DB 1; Length 129;
Best Local Similarity 66.2%; Pred. No. 1.95e-121;
Matches 88; Conservative 25; Mismatches 14; Indels 6; Gaps 4;

DB 1 METPAQLFLILLMLPDTGTGEIVLTQSPGTLSPGERATISCRASQSV--S-S--SYLA 55
1 MSQAQVLLILLWVSGTGDIVLTQSPDLSLGERATISCKSSQSLNSRRENTYA 60
QY 56 WYQKRGQAPRLIYAGASSRATGIPDRFSGSGGTDFLTLSRLEPEDFAVYYCOQYGS 115
61 WYQKRGQPKLLIYWASTRESGVDPDRFSGSGGTDFLTLSLQAEADVAVYYCTQ- SYN 119
DB 116 PWTFGGTVEIK 128
QY 120 LYTFGGTVEIK 132

RESULT 8
ID KV3L_HUMAN STANDARD; PRT; 129 AA.

AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION HAH PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 88171307.
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RT J. Exp. Med. 167:840-852(1988).
RL -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.

CC PIR; P10022; K3HUH1.
DR HSSP; P01789; 2MCP.
DR PFAM; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.

FT CHAIN 1 20
FT DOMAIN 21 129 IG KAPPA CHAIN V-II REGION HAH.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C552927274D0 CRC64;

Query Match 63.4%; Score 598; DB 1; Length 129;
Best Local Similarity 66.9%; Pred. No. 3.54e-121;
Matches 89; Conservative 25; Mismatches 13; Indels 6; Gaps 4;

DB 1 METPAQLFLILLMLPDTGTGEIVLTQSPGTLSPGERATISCRASQSV--S-S--SYLA 55
1 MSQAQVLLILLWVSGTGDIVLTQSPDLSLGERATISCKSSQSLNSRRENTYA 60
QY 56 WYQKRGQAPRLIYAGASSRATGIPDRFSGSGGTDFLTLSRLEPEDFAVYYCOQYGS 115
61 WYQKRGQPKLLIYWASTRESGVDPDRFSGSGGTDFLTLSLQAEADVAVYYCTQ- SYN 119
DB 116 PWTFGGTVEIK 128
QY 120 LYTFGGTVEIK 132

RESULT 9
ID KV3L_MOUSE STANDARD; PRT; 131 AA.

AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION MOPC 63 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE OF 1-35.
RX MEDLINE; 78235887.
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
the variable and constant regions of immunoglobulin light chain

RN		precursors: implications on the organization and controlled
RT		expression of immunoglobulin genes.";
RL	Biochemistry 17:2392-2400(1978).	
RN	[2]	
RP	SEQUENCE OF 21-131.	
RX	MEDLINE; 73140225.	
RA	McKean D.J., Potter M., Hood L.E.:	
RT	"Mouse Immunoglobulin chains. Pattern of sequence variation among	
RL	kappa chains with limited sequence differences."; Biochemistry 12:760-771(1973).	
RN	[3]	
RE	REVSIONS.	
RX	MEDLINE; 79012520.	
RA	McKean D.J., Bell M., Potter M.:	
RT	"Mechanisms of antibody diversity: multiple genes encode structurally	
RL	related mouse kappa variable regions."; Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).	
DR	PIR; A01935: KVM5M6.	
DQ	PPRM; PF00047; Ig; I.	
KW	Immunoglobulin V region; Signal.	
FT	SIGNAL	
FT	CHAIN 1 20	IG KAPPA CHAIN V-II REGION MOPC 63.
FT	DOMAIN 21 131	FRAMEWORK 1.
FT	DOMAIN 21 43	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 44 58	FRAMEWORK 2.
FT	DOMAIN 59 73	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 74 80	FRAMEWORK 3.
FT	DOMAIN 81 112	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN 113 121	FRAMEWORK 4.
FT	DISULFID 122 131	BY SIMILARITY.
FT	NON TER 43 112	
SO	SEQUENCE 131 AA; 14291 MW; D212EC9FD8C880A CRC64;	
	Query Match	61.9%; Score 584; DB 1; Length 131;
	Best Local Similarity	63.2%; Pred. No. 1.46e-117;
	Matches 84; Conservative 26; Mismatches 20; Indels 3; Gaps 3;	
Dq	1 METDTLLMLVILLWPSTGNTIVLTQSASLAVSLGGORATISCRASESV-DSYG-NSEFMH 58 ::: : ::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: 1 MDQAOVYLIILLMLWSVCGRDIVLTQSDSLAVSGERATISCSSOSLSRTEENTLYLA 60	
Dd	59 WYOOKPGPKPLTYLATNLNSGVPARSGGSRRDFFLITDPVAADAAHYCCONDD 118 :: 61 WYOKPQPPLPYIMASTRESVPDRFGSGSGGTDFLTTLISSLDADVAYCYTOST-Y 119	
Df	119 PWTEGGTGLEIK 131 :: ::	
Oy	120 LYTFQGCTKEVK 132	
RESULT 10		
ID	KV3H_HUMAN STANDARD; PRT; 129 AA.	
AC	P04207;	
DT	20-MAR-1987 (Rel. 04, Created)	
PT	01-MAY-1990 (Rel. 16, Last sequence update)	
DT	15-JUL-1999 (Rel. 38, Last annotation update)	
DS	IG KAPPA CHAIN V-III REGION CXL PRECURSOR (RHENMATOID FACTOR).	
OE	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo. [1]	
NP	SEQUENCE FROM N.A.	
RX	MEDLINE; 86177570.	
RA	Jirik F.R., Soreg J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P., Goldflen R., Carson D.A.:	
RT	"Cloning and sequence determination of a human rheumatoid factor light-chain gene"; Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986). -----	
Cc	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way	

```
CC modified and this statement is not removed. Usage by and for commercial/
CC entitled requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M12740; AAA58992.1; -
DR PIR; A01898; K3HUCI.
DR HSSP; P01789; 2MCP.
DR PFAM; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL
FT CHAIN 1
FT DOMAIN 21 129 43 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3-
FT DOMAIN 119 129 JKI SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;
Query Match 61.7%; Score 582; DB 1; Length 129;
Best Local Similarity 67.2%; Pred. No. 4,78e-117;
Matches 90; Conservative 21; Mismatches 15; Indels 8; Gaps 4;
Db 1 MEAPAQLLELLMLPDTTGETIMVTSPTATLSVSGERATLSCRASQSV--S---NN-LA 54
   ::::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 1 MDQAQAVILLTLWVSVCGRDVIITGSPDSLAVSLGERATLISCKSSQSGLNSTRRENTLA 60
Db 55 WYQQKPGPPRLILYGASTRATGIPARRSSGSSGGTEFLITLSRQSEPFAYTYCCQYNMW 114
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 61 WYQQKPGPPRLILYMASTRESGVDPDSGSSTGTFLTITSLOAEADVAVYYCYQSYN- 119
Db 115 PWTFPGSTGREIK 128
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 120 -LYTFGGSTGYEIK 132
RESULT 11
ID 11 KVLM_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85014148.
RA Klobbeck H.G., Combariato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on ways
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHOWK.
DR HSSP; P01607; IIREI.
DR PFAM; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL
FT CHAIN 1
FT DOMAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAWEWORK 1.
```

FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 71 71 FRAMEWORK 2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 79 110 FRAMEWORK 3.
 FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 120 129 FRAMEWORK 4.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA: 14069 MW: F941FA07DAFCA2F9 CRC64;

Query Match 58.68; Score 553; DB 1; Length 129;
 Best Local Similarity 65.7%; Pred. No. 1,39e-109;
 Matches 88; Conservative 18; Mismatches 19; Indels 9; Gaps 5;

Db 3 MRYPAOLLGLLMLGARC-DIQMTQSPSSLSASVGDRTYICRASQSY--S-----NYL 55
 1 MOSQAOVLTLILLWVSGT-CGDIVLTQSPDLSVLSGERATISCKSSQSLNRTRENTYL 59
 Db 56 MWYQKPGKAPKLLIYVAASLSQSVTSRFGSGSGTDFLTITSSLPEDSAFYVCOOYSTS 115
 60 MWYQKPGKAPKLLIYVAASLSQSVTSRFGSGSGTDFLTITSSLPEDSAFYVCOOYSTS 119
 Db 116 TLTFGQGTLEIK 129
 120 -LYTFGQGTLEIK 132

RESULT 12
 ID KV3K_HUMAN STANDARD; PRT; 128 AA.

AC P06311;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 RA Klobeck H.G., Melndi A., Combrilato G., Solomon A., Zachau H.G.;
 RT Human immunoglobulin kappa light chain genes of subgroups II and
 RL III.";
 Nucleic Acids Res. 13:6499-6513(1985).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: Z00021; CAA7316.1; -;
 DR PIR: A01899; K3H041.
 DR PFM: PF00047; 19; 1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 118 128 JKI SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 128 128
 SQ SEQUENCE 128 AA: 14070 MW: CC89570FE3B9012 CRC64;

Query Match 58.48; Score 551; DB 1; Length 128;
 Best Local Similarity 64.7%; Pred. No. 4,53e-109;
 Matches 86; Conservative 24; Mismatches 16; Indels 7; Gaps 5;

Db 1 MEMPAOLLFLMLPDTGTGIVLTQSPDTLSLSPESATLSCRASQSY--S--N-LA 54
 1 MOSQAOVLTLILLWVSGT-CGDIVLTQSPDLSVLSGERATISCKSSQSLNRTRENTYL 60
 Db 55 MWYQKPGKAPKLLIYVAASLSQSVTSRFGSGSGTDFLTITSSLPEDSAFYVCOOYSTS 114
 61 MWYQKPGKAPKLLIYVAASLSQSVTSRFGSGSGTDFLTITSSLPEDSAFYVCOOYSTS 119
 Db 115 PYTFGQGTLEIK 127
 120 LYTFGQGTLEIK 132

RESULT 13
 ID KV3K_HUMAN STANDARD; PRT; 116 AA.

AC P04434;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION VH PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85087932.
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus.";
 RL Nucleic Acids Res. 12:9229-9236(1984).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: X02725; -, NOT_ANNOTATED_CDS.
 DR PIR: A01901; K3H0VH.
 DR HSSP: P01789; ZMCP.
 DR PFM: PF00047; 19; 1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 177 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA: 12757 MW: 51CD55BA3B21929 CRC64;

Query Match 56.7%; Score 535; DB 1; Length 116;
 Best Local Similarity 64.2%; Pred. No. 5,76e-105;
 Matches 77; Conservative 24; Mismatches 14; Indels 5; Gaps 3;

Db 1 MEAPPAOLLFLMLPDTGTREIVMTQSPDTLSLSPGERVTLSCRASQSY--S--SYLT 55
 1 MOSQAOVLTLILLWVSGT-CGDIVLTQSPDLSVLSGERATISCKSSQSLNRTRENTYL 60
 Db 56 MWYQKPGKAPKLLIYVAASLSQSVTSRFGSGSGTDFLTITSSLPEDSAFYVCOOYSTS 115
 61 MWYQKPGKAPKLLIYVAASLSQSVTSRFGSGSGTDFLTITSSLPEDSAFYVCOOYSTS 120

RESULT 14
 ID KV2E_HUMAN STANDARD; PRT; 117 AA.
 AC P06309;

```

DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION GM607 PRECUSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84191506.
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity."
RL Nature 309:73-76(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC
CC EMBL: Z00009; -; NOT_ANNOTATED_CDS.
DR PIR: A01889; K2HUGM.
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK 1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 58 FRAMEWORK 2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 66 97 FRAMEWORK 3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 107 116 FRAMEWORK 4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match
Best Local Similarity 56.7%; Score 535; DB 1; Length 117;
Matches 81; Conservativity 13; Mismatches 21; Indels 2; Gaps 2;

DB 1 GSSGDIWYTGSPSLPYPGPAPISCRSSQSLHSNG-YNYLDWYLOKPOQSPQLIYL 59
QY 17 GTCGDIVLTGSPDSLAVSLGERATISCKSSQSLNSRTRENYLAWYQKPPQPKLIYW 76
DB 60 GSNRAGVDPDRFSGSGGTDETLKISRNEADGVYCMOGLQTPQFGQGTKEIK 116
QY 77 ASTRESGVDPDRFSGSGGTDETLTISLQADVAVYCTOSYNL-YTFGGGTKEIK 132

RESULT 15
ID KY3P.MOUSE STANDARD; PRT; 110.AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RP SEQUENCE.
RX MEDLINE: 79073152.
RA Weigert M., Gatmaitan L., Ioh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."
RL Nature 276:785-790(1978).
DR PIR: D01937; KVM510.
DR PFAM: PF00047; 1g; 1.

```

```

KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 101 110 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CEB86B1249 CRC64;

Query Match
Best Local Similarity 56.6%; Score 534; DB 1; Length 110;
Matches 79; Conservativity 12; Mismatches 19; Indels 2; Gaps 2;

DB 1 DIVTQSPASLAVSLGPRATISCKASQSL-DYDG-DSYNNWYQKPPQPKLIYASNL 58
QY 21 DIVTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLAWYQKPPQPKLIYMASTR 80
DB 59 ESGIPARFSGSGGTDETLNHPVEEDATYVYCHOSEDPWTGSGTKLEIK 110
QY 81 ESGVDPDRFSGSGGTDETLTISLQADVAVYCTOSYNL-YTFGGGTKEIK 132

Search completed: Mon Aug 7 19:02:14 2000
Job time : 9 secs.

```

 Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

 (TM)

 Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

Msrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 7 19:02:32 2000; Maspar time 17.93 Seconds

Tabular output not generated. 510.526 Million cell updates/sec

Title: >US-09-249-011-8
 Description: (1-132) from US09249011.pep
 Perfect Score: 943
 Sequence: 1 MDSQAVLLILLMLWVGTCG.....YCTQSYNLYTFQGTVEIK 132

Scoring table: PAM 150
 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: sptrembl12

1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
 5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
 9:sp.phase 10:sp.plant 11:sp.protein 12:sp.unclassified
 13:sp.vertebrate 14:sp.virus

Statistics: Mean 41.466; Variance 66.918; scale 0.620

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	185	19.6	123	11	061243 8HS20 PROTEIN PRECURSOR	5.81e-19
2	164	17.4	100	6	077624 SURROGATE LIGHT CHAIN	1.38e-14
3	129	13.7	509	11	008907 BRAIN IMMUNOLOGICAL-I	1.05e-07
4	124	13.1	513	11	P97797 PROTEIN TYROSINE PHOSP	8.91e-07
5	123	13.0	122	4	099604 TRGV9 (FRAGMENT)	1.36e-06
6	123	13.0	122	4	099603 TRGV9 (FRAGMENT)	1.36e-06
7	120	12.7	210	6	P79336 CD8 BETA ANTIGEN PRECU	4.80e-06
8	119	12.6	509	11	09WTN4 BIT.	7.29e-06
9	118	12.5	81	4	075734 IG HEAVY CHAIN VARIAB	1.10e-05
10	113	12.0	150	4	095973 VH4 HEAVY CHAIN VARIAB	8.58e-05
11	113	12.0	198	4	013970 CD8 ANTIGEN	8.58e-05
12	113	12.0	235	6	09XSM6 CD8 ALPHA CHAIN PRECUR	8.58e-05
13	111	11.8	169	4	09Y2N4 T-CELL RECEPTOR V-GAM	1.92e-04
14	110	11.7	81	4	075736 IG HEAVY CHAIN VARIAB	2.87e-04
15	110	11.7	82	4	075732 IG HEAVY CHAIN VARIAB	2.87e-04
16	107	11.3	77	4	075726 IG HEAVY CHAIN VARIAB	9.45e-04
17	106	11.2	74	4	075744 IG HEAVY CHAIN VARIAB	1.40e-03
18	106	11.2	82	4	075725 IG HEAVY CHAIN VARIAB	1.40e-03
19	106	11.2	150	4	091298 IGG VH PROTEIN PRECURS	1.40e-03
20	106	11.2	318	13	091664 CORTICAL THYMOCYTE MAR	1.40e-03

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
21	105	11.1	81	4	075721 IG HEAVY CHAIN VARIAB	2.07e-03
22	103	10.9	346	4	060781 DA232G24.1	2.07e-03
23	103	10.9	147	4	09Y509 VH3 PROTEIN (FRAGMENT)	4.50e-03
24	102	10.8	77	4	075741 IG HEAVY CHAIN VARIAB	6.60e-03
25	102	10.8	167	13	P79985 CD8 ALPHA CHAIN (FRAGM	6.60e-03
26	102	10.8	167	13	P79985 CD8 ALPHA CHAIN (FRAGM	6.60e-03
27	102	10.8	1142	4	060732 MELANOMA-ASSOCIATED AN	6.60e-03
28	102	10.8	1142	4	060732 CANCER/TESTIS ANTIGEN	6.60e-03
29	99	10.5	118	11	075739 IG HEAVY CHAIN VARIAB	2.06e-02
30	97	10.3	118	11	0921C4 ANTI-PORCINE VCAM MAB	4.36e-02
31	97	10.3	200	4	095776 H.NH1021A08.2 PROTEIN	4.36e-02
32	97	10.3	209	6	09XSM7 CD8 ALPHA CHAIN PRECUR	4.36e-02
33	97	10.3	235	13	090770 CD8 ALPHA CHAIN PRECUR	4.36e-02
34	97	10.3	272	11	070356 BUTYROPHILIN-LIKE (FRA	4.36e-02
35	97	10.3	288	4	000517 HPD-1.	4.36e-02
36	96	10.2	75	4	075743 IG HEAVY CHAIN VARIAB	6.32e-02
37	96	10.2	78	4	075723 IG HEAVY CHAIN VARIAB	6.32e-02
38	96	10.2	259	4	095532 DJ889N15.1 (NOVEL PROT	6.32e-02
39	96	10.2	506	6	046631 MYD-1 ANTIGEN PRECURSO	6.32e-02
40	96	10.2	4162	13	098918 CONNECTIN/TITIN (FRAGM	6.32e-02
41	96	10.2	5198	5	076518 HEMICENTIN PRECURSOR	6.32e-02
42	95	10.1	86	4	075740 IG HEAVY CHAIN VARIAB	9.13e-02
43	95	10.1	97	4	043234 RHEUMATOID FACTOR RP-E	9.13e-02
44	95	10.1	401	6	008835 POLIOVIRUS RECEPTOR AL	9.13e-02
45	94	10.0	16	14	079458 LIGHT-CHAIN COMPLEMENT	1.32e-01

ALIGNMENTS

RESULT 1
 ID 061243 PRELIMINARY; PRT; 123 AA.

DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)

DE 8HS20 PROTEIN PRECURSOR.
 GN VPRED3.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NP [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE: 93259124.

RA SHIRASAKA T., OHNISHI K., HAGIWARA S., SHIGEMOTO K., TAKEBE Y.,
 RA RALEWSKY K., TAKEMOTO T.,
 RT "A novel gene product associated with mu chains in immature B cells."

RL EMBL J. 12:1827-1834(1993).
 DR EMBL: D13208; BAA02495.1; .

DR MGD: MGI:98938; Vpred3.

DR PFM: PFM0047; 19; 1.
 FT CHAIN

FT SEQUENCE 123 AA; 13400 MW; DA2A70D3 CRC32;
 8HS20 PROTEIN.

Query Match 19.6%; Score 185; DB 11; Length 123;
 Best Local Similarity 36.3%; Pred. No. 5.81e-19;
 Matches 41; Conservative 28; Mismatches 36; Indels 8; Gaps 6;

Db 7 LPLLIGTFVAVFQPTLQ-PDAFSVFPQDAHUSC-TINSQ-HATAGDIGSVYQOQPG 63
 OY 8 LILLILWWSGTCGDIYVLQSPDSLAVSGERATISCKSSQSLNSRTENTLANTYQOQPG 67

Db 64 SAPHLILTYAEERHYPADIPDRSATYDAAHNACILTISVLPEDDADYFCS 116
 OY 68 QPKKILTYMAST---RESGVDFRSGSGSGT-DF-TLTISSLOAEVAVYVCT 115

Db 64 SAPHLILTYAEERHYPADIPDRSATYDAAHNACILTISVLPEDDADYFCS 116
 OY 68 QPKKILTYMAST---RESGVDFRSGSGSGT-DF-TLTISSLOAEVAVYVCT 115

Db 64 SAPHLILTYAEERHYPADIPDRSATYDAAHNACILTISVLPEDDADYFCS 116
 OY 68 QPKKILTYMAST---RESGVDFRSGSGSGT-DF-TLTISSLOAEVAVYVCT 115

Db 64 SAPHLILTYAEERHYPADIPDRSATYDAAHNACILTISVLPEDDADYFCS 116
 OY 68 QPKKILTYMAST---RESGVDFRSGSGSGT-DF-TLTISSLOAEVAVYVCT 115

Db 64 SAPHLILTYAEERHYPADIPDRSATYDAAHNACILTISVLPEDDADYFCS 116
 OY 68 QPKKILTYMAST---RESGVDFRSGSGSGT-DF-TLTISSLOAEVAVYVCT 115

Db 64 SAPHLILTYAEERHYPADIPDRSATYDAAHNACILTISVLPEDDADYFCS 116
 OY 68 QPKKILTYMAST---RESGVDFRSGSGSGT-DF-TLTISSLOAEVAVYVCT 115

Db 64 SAPHLILTYAEERHYPADIPDRSATYDAAHNACILTISVLPEDDADYFCS 116
 OY 68 QPKKILTYMAST---RESGVDFRSGSGSGT-DF-TLTISSLOAEVAVYVCT 115

Db 64 SAPHLILTYAEERHYPADIPDRSATYDAAHNACILTISVLPEDDADYFCS 116
 OY 68 QPKKILTYMAST---RESGVDFRSGSGSGT-DF-TLTISSLOAEVAVYVCT 115

Db 64 SAPHLILTYAEERHYPADIPDRSATYDAAHNACILTISVLPEDDADYFCS 116
 OY 68 QPKKILTYMAST---RESGVDFRSGSGSGT-DF-TLTISSLOAEVAVYVCT 115

```

DE SURGATE LIGHT CHAIN (FRAGMENT).
GN VPREB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RA RAYCHEL A.P., HALLIGAN B.D.;
RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF068848; AAC19380.1; -.
DR HSSP: P01703; 7FAB.
FT NON_TER 1
FT NON_TER 100
SQ SEQUENCE 100 AA; 11142 MW; 3785537C CRC32;

Query Match
Best Local Similarity 38.2%; Pred. No. 1,38e-14;
Matches 39; Conservative 19; Mismatches 34; Indels 10; Gaps 9;

Db 3 LILHRGCGSPYLSQP-SVASFGLATYRLACTLSSDH-DVNLHSIT--WTQQRPHRP 58
Qy 11 LILWVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENTLYAMTQKPGQPP 70
Db 59 RFLRYFSPDKRGHVPDRFSGSKDLAKNTGYLSIAELQA 100
Qy 71 K-LLIYMA-S-TRES-GVPDRFSGSGS-GTDPT-LTISLQA 106

RESULT 3
ID 008907 PRELIMINARY; PRT: 509 AA.
AC 008907;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DI 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE BRAIN IMMUNOLOGICAL-LIKE PROTEIN (BIT).
GN BIT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE: 97230468.
RA OHNISHI H., KUBOTA M., SANO S.;
RT "BIT (Bit) maps to mouse chromosome 2.";
RL Genomics 40:504-506(1997).
DR EMBL: D85785; BAA20376.1; -.
DR MGD: MGI:107947; Bit.
DR PFM: PF00047; Ig 3.
SQ SEQUENCE 509 AA; 56033 MW; 4C020C08 CRC32;

Query Match
Best Local Similarity 28.4%; Pred. No. 1,05e-07;
Matches 29; Conservative 32; Mismatches 31; Indels 10; Gaps 10;

Db 27 TGATGTEVVTQPEKSVSAAGDSTILNCTV- SIL-P-V-GP-IMYRG-VGQS-RLII 79
Qy 16 SCGCG-DIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENTLYAMTQKPGQPPKLLI 74
Db 80 YSTGEHPFVRNVSDPTKRNNDFFSIRISNVTPEADAGTYIC 121
Qy 75 Y-WASTRESGVDPDRFSGSG-SGTDFTLTITSLQAEVAVTYIC 114

RESULT 4
ID P97797 PRELIMINARY; PRT: 513 AA.
AC P97797; P97796: Q35924; Q88555; Q88556;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DI 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DI 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR

```

```

DE (P84) (SHP SUBSTRATE-1) (INHIBITORY RECEPTOR SHPS-1) (SHPS1).
PTPNS1 OR P84 OR SHPS-1 OR SHPS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 97223399.
RA YAMAO T., MATOZAKI T., AMANO K., MATSUDA Y., TAKAHASHI N., OCHI F.,
RA FUKIOKA Y., KASUGA M.;
RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
RT localization of genes.";
RL Biochem. Biophys. Res. Commun. 231:61-67(1997).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-53; 422-424 AND 429-433.
RC STRAIN-BALB/C; TISSUE-CEREBELLUM, AND BRAIN;
RX MEDLINE: 98012243.
RA COMU S., MENG W., OLINSKY S., ISHMAD P., MI Z., HEMPFL J., WATKINS S.,
RA LAGENAUR C.F., NARAYANAN V.;
RT "The murine P84 neural adhesion molecule is SHPS-1, a member of the
RT phosphatase-binding protein family.";
RL J. Neurosci. 17:8702-8710(1997).
RN [3]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC STRAIN-C57BL/6; TISSUE-FETAL THYMUS;
RX MEDLINE: 98380500.
RA VEILLETTE A., THIBAUDEAU E., LATOUR S.;
RT "High expression of inhibitory receptor SHPS-1 and its association
RT with protein tyrosine phosphatase SHP-1 in macrophages.";
RL J. Biol. Chem. 273:22719-22728(1998).
RN [4]
RP FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX MEDLINE: 90152134.
RA CHUANG W., LAGENAUR C.F.;
RT "Central nervous system antigen P84 can serve as a substrate for
RT neurite outgrowth.";
RL Dev. Biol. 137:219-232(1990).
RN [5]
RP FUNCTION: BINDS TO THE SH2 DOMAINS OF PROTEIN-TYROSINE PHOSPHATASE
2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY VARIOUS
MITOGENS AND CELL ADHESION. PROTEIN SUPPORTS ADHESION OF
CEREBELLAR NEURONS, NEURITE OUTGROWTH AND GLIAL CELL ATTACHMENT.
MAY PLAY A KEY ROLE IN INTRACELLULAR SIGNALING DURING
SYNAPTONEGENESIS AND IN SYNAPTIC FUNCTION. MAY ACT AS A DOCKING
PROTEIN AND INDUCE TRANSLOCATION OF SHP-2 FROM THE CYTOSOL TO THE
PLASMA MEMBRANE; TYROSINE PHOSPHORYLATED PTPNS1 FROM MACROPHAGES
PRIMARILY ASSOCIATES WITH SHP-1.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THREE FORMS: ISOFORMS 1 (SHOWN HERE), 2 AND
SMALL, ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE CEREBRAL CORTEX, CEREBELLUM,
SPINAL CORD, SPLEEN AND MACROPHAGES AND AT MUCH LOWER LEVEL IN THE
KIDNEY, HEART, LIVER AND THYMUS. WITHIN THE CEREBELLUM, EXPRESSION
IS DETECTED IN THE SYNAPTIC GLOMERULI, GRANULE CELL BODIES, GOLGI
EPITHELIAL CELLS, OLFACTORY BULB, NEURONS IN THE HIPPOCAMPUS AND
THE DENTATE GYRUS. IN THE EYE, EXPRESSION IS FIRST SEEN IN THE
INNER PLEXIFORM AND OPTIC FIBER LAYERS, LATER IN DEVELOPMENT
EXPRESSION IS ALSO SEEN IN THE OUTER PLEXIFORM, RETINA AND OUTER
SEGMENTS OF THE PHOTORECEPTOR LAYER.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 7, WHEN
EXPRESSION IS RESTRICTED TO THE FLOOR PLATE REGION OF THE VENTRAL
NEURAXIS. WIDESPREAD EXPRESSION IN A VARIETY OF CNS REGIONS BEGINS
2-5 DAYS AFTER BIRTH.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
TWO CI-LIKE AND ONE V-LIKE DOMAINS.
DR EMBL: D87968; BAA13521.1; -.
DR EMBL: D87967; BAA13520.1; -.
DR EMBL: U89694; AAB92591.1; -.
DR EMBL: AF072543; AAC24886.1; -.
DR EMBL: AF072544; AAC24887.1; -.
DR MGD: MGI:108563; Ptpns1.
DR PFM: PF00047; Ig 3.
KW Signal, Transmembrane, Alternative splicing, Immunoglobulin domain;

```

RefSeq	Protein	Position	AA	Score	DB	Length	Indels	Gaps
KM	Glycoprotein: SH3-binding; Phosphorylation.	1	513	13.1%	DB 11;	513;		
FT	CHAIN	32	513					
FT	DOMAIN	32	373					
FT	TRANSMEM	374	394					
FT	DOMAIN	395	513					
FT	DOMAIN	51	124					
FT	DOMAIN	167	234					
FT	DOMAIN	270	336					
FT	DOMAIN	440	443					
FT	DOMAIN	450	456					
FT	DOMAIN	464	467					
FT	DOMAIN	481	484					
FT	DOMAIN	505	508					
FT	MOD_RES	423	423					
FT	MOD_RES	440	440					
FT	MOD_RES	464	464					
FT	MOD_RES	481	481					
FT	MOD_RES	505	505					
FT	MOD_RES	54	54					
FT	CARBOHYD	92	92					
FT	CARBOHYD	168	168					
FT	CARBOHYD	180	180					
FT	CARBOHYD	205	205					
FT	CARBOHYD	209	209					
FT	CARBOHYD	246	246					
FT	CARBOHYD	271	271					
FT	CARBOHYD	293	293					
FT	CARBOHYD	302	302					
FT	CARBOHYD	312	312					
FT	CARBOHYD	320	320					
FT	CARBOHYD	345	345					
FT	CARBOHYD	367	367					
FT	VARSPLIC	147	364					
FT	VARSPLIC	425	428					
FT	CONFLICT	10	10					
FT	CONFLICT	29	29					
FT	CONFLICT	67	67					
FT	CONFLICT	74	74					
FT	CONFLICT	83	83					
FT	CONFLICT	86	87					
FT	CONFLICT	90	90					
FT	CONFLICT	91	91					
FT	CONFLICT	96	96					
FT	CONFLICT	114	114					
FT	CONFLICT	118	118					
FT	CONFLICT	126	127					
FT	CONFLICT	128	128					
FT	CONFLICT	194	194					
FT	CONFLICT	224	224					
FT	CONFLICT	351	351					
FT	CONFLICT	365	365					
FT	CONFLICT	490	490					
SO	SEQUENCE	513 AA;	56425 MW;					
			0E29251A CRC32;					
Query Match	Similarity	13.1%;	Score 124;	DB 11;	Length 513;			
Best Local	Similarity	28.4%;	Pred. No. 8.91e-07;					
Matches	Conservative	29;	Mismatches	31;	Indels	10;	Gaps	10;
Db	27	TCGYGKELKATQPEKSVSAAGDSIVLNCILT-SLL-P-V-GP-IKWTRG-VGQS-RLII 79						
QY	16	SGTGG-DIVLQSPDSLAVSLGEERATICKSSOSLNSRTRENTLAWYQGRKGPCKILLI 74						
Ddb	80	YSTGEHPRPTVNSDAFKRNMPDSISIVTPEADGATYYC 121						

```

ID RESULT      5 PRELIMINARY; PRT; 122 AA.
AC Q99604.
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE TRGV9. (FRAGMENT).
GN
OS Homo sapiens (Human)..
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RA LEFRANC M.P.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90033295.
RA DARIAVACH P., LEFRANC M.P.;
RT "The promoter regions of the T-cell receptor V9 gamma (TRGV9) and V2
RL delta (TRVD2) genes display short direct repeats but no TAAT box.";
RN [3]
RP SEQUENCE FROM N.A.
RA LEFRANC M.P.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X15774; CAA3345.1; -.
DR HSSP; P80362; IWTL.
DR PFAM; PF00047; I9; 1.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13441 MW; C07D3DB9 CRC32;

Query Match 13.0%; Score 123; DB 4; Length 122;
Best Local Similarity 37.1%; Pred. No. 1.36e-05;
Matches 23; Conservative 16; Mismatches 16; Indels 7; Gaps 6

Db 117 CA 118
QY 114 CT 115

RESULT      6 PRELIMINARY; PRT; 122 AA.
AC Q99603;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE TRGV9. (FRAGMENT).
GN TRGV9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RA LEFRANC M.P.;
RX MEDLINE; 88283640.
RA HUCK S., DARIAVACH P., LEFRANC M.P.;
RT "Variable region genes in the human T-cell rearranging gamma (TRG)
RL locus: V-J junction and homology with the mouse genes.";
RN EMBO J. 7:719-726(1988).
[2]
RP SEQUENCE FROM N.A.
RA LEFRANC M.P.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X07205; CAA30181.1; -.
DR HSSP; P80362; IWTL.
DR PFAM; PF00047; I9; 1.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13414 MW; E1CCA59F CRC32;
```

```

Query Match 13.0%; Score 123; DB 4; Length 122;
Best Local Similarity 37.1%; Pred. No. 1.36e-06;
Matches 23; Conservative 16; Mismatches 16; Indels 7; Gaps 6;

Db 57 WYRERPEVIOFLVSIISYDGTREKESGIPSGKFEVDRIPEPSTLTIHNVEKODIATVY 116
|:::|::: | |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Oy 61 WYQKPGPRL--I-YMASTR-ESGVPD-RFS-GSSGSTD-PTLISSIQADVAIVY 113
|:
Db 117 CA 118
|:
Oy 114 CT 115

RESULT 7 PRELIMINARY; PRT; 210 AA.
ID P79336 AC P79336;
DC 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE CDB BETA ANTIGEN PRECURSOR.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA MIYAZAWA T.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RX MEDLINE; 97067796.
RA PECORARO M.R., SHIMOJIMA M., MAEDA K., INOSHITA Y., KAWAGUCHI Y.,
RA KAI C., MIKAMI T.;
RT "Molecular cloning of the feline CD8 beta-chain.";
RL Immunology 89:84-88(1996).
DR EMBL; AB000484; BAA19125.1; -.
DR PFM; PF00047; 19; 1.
KW Signal.
FT SIGNAL. 1 21 POTENTIAL.
FT CHAIN 22 210 POTENTIAL.
FT CHAIN 22 210 POTENTIAL.
SQ SEQUENCE 210 AA; 23105 MM; 915E2BD1 CRC32;

Query Match 12.7%; Score 120; DB 6; Length 210;
Best Local Similarity 27.2%; Pred. No. 4.80e-06;
Matches 37; Conservative 32; Mismatches 56; Indels 11; Gaps 9;

Db 2 OPGLLLATATGALRGSSVLOQAAGSVYVQTNGWIVISCARKTSP-TS-TRIYWL-RHR 58
|:|:|:|: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Oy 4 QAOYIILLIWMVSGCGSIGVLTQSPDSLAVSLGEPATISCSASSLSNRREYTLAWYQ 63
59 QAPSDSHYECLAWDPPIKGIYVGOEVEPEKLTVPDPATRSILNLVSKPADSGIYECMT 118
|:|:|:|: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Oy 64 QKPGPRL--LIYASTRE-S-G--V-PDFSGSGSGTDTLTLISSIQADVAIVY-C-T 115
119 VGSPELTIFGKTRLSV 134
|:|:|:|: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Oy 116 QSYNLYTEFGOGTKEVI 131

RESULT 8 PRELIMINARY; PRT; 509 AA.
ID Q9WTN4 AC Q9WTN4;
DC 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE BIT.
GN BIT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

```

[illegible]

SO	SEQUENCE	235 AA;	25728 MW;	F22E0AB5 CRC32;
Db	55 SWLQKRCGAASPFLLYLISOTRKRVADGDLDAQKFSGSKMKGDSFTLLRDFRERDQGFYF	114		
Qy	60 AM-YQOK-PGQPKLLIY-MAST-R-ESGV-PDRFSGSGOTDETLTIRISSIQAEADVY	113		
Db	115 CS 116			
Qy	114 CT 115			
RESULT	13	PRELIMINARY;	PRT;	169 AA.
ID	09Y2N4			
AC	09Y2N4;			
DT	01-NOV-1998 (TREMBlrel. 12, Created)			
DT	01-NOV-1998 (TREMBlrel. 12, Last sequence update)			
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)			
DE	T-CELL RECEPTOR V-GAMMA 8.			
GN	H.NH1021A08.4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 99063792.			
RA	SULSTON J.E., WATERSTON R.;			
RT	"toward a complete human genome sequence.";			
RL	Genome Res. 8:1097-1108(1998).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RP	ARNETT C., MOHLMANN P., LE T.;			
RT	"The sequence of Homo sapiens BAC clone NH0121A08.";			
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RP	WATERSTON R.H.;			
RA	WATERSTON R.H.;			
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RP	WATERSTON R.;			
RA	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AC006033; AAD15555.1; -.			
KW	Receptor.			
SO	SEQUENCE	169 AA;	18958 MW;	D061B665 CRC32;
Query Match		11.8%;	Score 111;	DB 4; Length 169;
Best Local Similarity		29.2%;	Pred. No. 1.92e-04;	
Matches	19;	Conservative	20;	Mismatches 19; Indels 7; Gaps 5
Db	50 YTHWYLHOEGKAPORLLYDYSNRVLESGISSEKHYTAAGTSLKFTILENIERDSC	109		
Qy	58 YLAWQKPGQOP-KLLIYMA-STR---ESGVP-DRFSG-SGSGTDETLTIRISSIQAEADVA	110		
Db	110 VYCYA 114			
Qy	111 VYCT 115			
RESULT	14	PRELIMINARY;	PRT;	81 AA.
ID	075736			
AC	075736;			
DT	01-NOV-1998 (TREMBlrel. 08, Created)			
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)			
DT	01-NOV-1998 (TREMBlrel. 08, Last annotation update)			
DE	IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
GN	VH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.			

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE:
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ009534; CAA08740.1; -
 FT NON_TER 1 1
 FT NON_TER 81 81
 SQ SEQUENCE 81 AA; 9375 MW; C233614E CRC32;

Query Match 11.7%; Score 110; DB 4; Length 81;
 Best Local Similarity 33.3%; Pred. NO.2.87e-04;
 Matches 17; Conservative 13; Mismatches 17; Indels 4; Gaps 4;

Db 27 Y-ATAIASVGRFTISRDSKNMFLQMSLKKEEDAVYICV-AYEGYY 75
 75 YMASTRSGVDFRFS-GSGSGTDFL-LTISSLQAEADVAVYYCTOSYNLYTF 123

RESULT 15
 ID 075732 PRELIMINARY; PRT; 82 AA.
 AC 075732;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE:
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ009534; CAA08736.1; -
 DR HSSP; P01772; 2IG2.
 FT NON_TER 1 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 9387 MW; 440D63F2 CRC32;

Query Match 11.7%; Score 110; DB 4; Length 82;
 Best Local Similarity 33.8%; Pred. NO.2.87e-04;
 Matches 24; Conservative 17; Mismatches 23; Indels 7; Gaps 7;

Db 1 YMDVVRQAPGKLEWVSVIFASGSIYYADSVKGRFVSRDTSKNTLFLQMSLRAEDTAV 60
 QY 58 YLAVYQOKPGQPK-L-LIY-WASIR-ESGVDFRSGS-GSGTD-FTLISLQAEADVAV 111
 Db 61 YYCARDITGLY 71
 QY 112 YYCTQ-SYNLY 121

Search completed: Mon Aug 7 19:02:53 2000
 Job time : 21 secs.

 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution Rights by Oxford Molecular Ltd

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 7 19:03:42 2000; Maspar time 9.71 Seconds

Tabular output not generated. 322.033 Million cell updates/sec

Title: >US-09-249-011-8
 Description: (1-132) from US09249011.pep
 Perfect Score: 943
 Sequence: 1 MDSQAOVILILLMWVSGTGC.....YCTQSYNTYTFGGTKEIK 132

Scoring table: PAM 150
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq36
 l-geneseqp

Statistics: Mean 30.911; Variance 170.801; scale 0.181

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	819	86.9	148	1	P93078	1.28e-51
2	818	86.7	239	1	R76087	1.52e-51
3	803	85.2	137	1	W10545	2.11e-50
4	797	84.5	137	1	W10544	6.05e-50
5	777	82.4	133	1	R59509	Sequence of the light
6	770	81.7	133	1	P80894	Sequence of L chain of
7	768	81.4	134	1	W06206	Xenograft antibody HAK
8	762	80.8	133	1	R85909	Monoclonal antibody, C
9	756	80.2	241	1	R28809	Vector PMDR1007.
10	751	79.6	137	1	W10547	Wild type murine anti-
11	748	79.3	133	1	R48633	Sequence of Hum4V, gen
12	744	78.9	137	1	W21655	Chimeric Mab 15 PCR mo
13	744	78.9	139	1	R94669	Monoclonal antibody PA
14	743	78.8	134	1	R30485	V kappa region of Ab t
15	741	78.6	137	1	W21653	Mouse Mab 15 light cha
16	737	78.2	134	1	R25158	V-region of L-chain of
17	731	77.5	134	1	R38317	Sequence encoded by th
18	698	74.0	133	1	R59511	Sequence of the light
19	697	73.9	495	1	Y06908	CARAB-TEV amino acid se
20	697	73.9	495	1	W32480	Growth factor CARAB-TE
21	693	73.5	134	1	R81838	E-selectin-specific an
22	691	73.3	134	1	R81841	E-selectin CDR-grafted
23	686	72.7	155	1	Y06912	Human variable kappa 1

ID	Query Match	Score	Length	ID	Description	Pred. No.
24	686	72.7	155	1	W22483	Kappa light chain vari
25	686	72.7	342	1	Y06909	TuH1 amino acid sequen
26	686	72.7	342	1	W22482	Growth factor TuH1 (ca
27	683	72.4	131	1	R53533	DREB-200 Ab light chai
28	676	71.7	171	1	R30144	Mab GAH variable regio
29	676	71.7	171	1	R38320	Sequence of signal pep
30	676	71.7	274	1	R38319	Sequence of Hum4 VL-CC
31	676	71.7	284	1	R38321	Sequence of PSC49FLAG.
32	675	71.6	113	1	R50314	Humanised light chain
33	673	71.4	113	1	W27346	Human Ab light chain v
34	668	70.8	113	1	R50313	Humanised light chain
35	666	70.6	285	1	R48638	Sequence of plasmid ps
36	665	70.5	114	1	Y06830	Mouse Mab 6A4 light ch
37	664	70.4	219	1	R76086	Mab 55.1 light chain.
38	663	70.3	249	1	W60770	Single chain antibody
39	660	70.0	133	1	R55555	DREB-200 Humanized ant
40	660	70.0	288	1	W82743	Fusion protein PNG4/55
41	660	70.0	673	1	W82742	Plasmid PNG4/55.1scfv/
42	659	69.9	111	1	R52059	Light chain variable r
43	654	69.4	114	1	R45605	Monoclonal antibody GP
44	654	69.4	114	1	W15537	Anti-TGF beta-1 scfv a
45	648	68.7	120	1	R61240	Monoclonal antibody L6

ALIGNMENTS

RESULT 1
 ID P93078 standard; peptide; 148 AA.
 AC P93078;
 DT 14-MAR-1990 (first entry)
 DE Light chain of monoclonal antibody 6A4.
 KW Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.
 PN EP-338395-A.
 PD 25-OCT-1989.
 PF 12-APR-1989; 106463.
 PR 19-APR-1988; DE-813023.
 PA (BEHW) Behringwerke.
 PI Domdey H, Marget M, von Specht BU;
 DR WPT: 89-310861/43.
 DR N-PSDB; N91663.
 PT Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
 PT variable antibody regions.
 PS Claim 1; page 6; 7pp; german.
 CC The peptide is encoded by the light chain of monoclonal antibody 6A4.
 CC 6A4 reacts with the OMP-1 protein of all 19 known serotypes of
 CC P.aeruginosa. It is used for therapy and diagnosis of infection, and as
 CC a carrier for drugs. The antibody is IgG2a subclass.
 SQ Sequence 148 AA;

Query Match 86.9%; Score 819; DB 1; Length 148;
 Best Local Similarity 86.4%; Pred. No. 1.28e-51;
 Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

ID	Query Match	Score	Length	ID	Description	Pred. No.
Db	1	819	148	1	P93078	1.28e-51
Oy	1	819	148	1	P93078	1.28e-51
Db	61	751	137	1	W10547	1.90e-46
Oy	61	751	137	1	W10547	1.90e-46
Db	121	744	139	1	R94669	6.47e-46
Oy	121	744	139	1	R94669	6.47e-46
Db	121	743	134	1	R30485	7.71e-46
Oy	121	743	134	1	R30485	7.71e-46
Db	121	741	137	1	W21653	1.09e-45
Oy	121	741	137	1	W21653	1.09e-45
Db	121	737	134	1	R25158	2.20e-45
Oy	121	737	134	1	R25158	2.20e-45
Db	121	731	134	1	R38317	6.28e-45
Oy	121	731	134	1	R38317	6.28e-45
Db	121	698	133	1	R59511	2.00e-42
Oy	121	698	133	1	R59511	2.00e-42
Db	121	697	495	1	Y06908	2.38e-42
Oy	121	697	495	1	Y06908	2.38e-42
Db	121	697	495	1	W32480	4.78e-42
Oy	121	697	495	1	W32480	4.78e-42
Db	121	693	134	1	R81838	6.77e-42
Oy	121	693	134	1	R81838	6.77e-42
Db	121	691	134	1	R81841	6.77e-42
Oy	121	691	134	1	R81841	6.77e-42
Db	121	686	155	1	Y06912	1.62e-41
Oy	121	686	155	1	Y06912	1.62e-41

RESULT 2
 ID R76087 standard; protein; 239 AA.
 AC R76087;
 DT 21-NOV-1995 (first entry)
 DE Mab 55.1 light chain.
 KW Antigen binding structure; complementarity determining region; CDR;
 KW Antigen binding structure; complementarity determining region; CDR;
 KW CA5.1; colorectal cancer; tumor-associated antigen; hybridoma;

KW monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;
 KW transgenic animal; transgenic plant; antibody engineering;
 KW humanized antibody; immunotoxin.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT peptide 1..20
 FT /label= Sig_peptide
 FT 21..239
 FT protein /label= Mat_protein
 FT /note= "Claim 3, page 98"
 PN W09515382-A.
 PD 08-JUN-1995.
 PF 29-NOV-1994; G02610.
 PR 03-DEC-1993; GB-024819.
 PR 03-JUN-1994; GB-011089.
 PA (ZENE) ZENECA LTD.
 PI Blaisey DC, Boot C, Copley CG, Hall SM, Paterson DS;
 PI Rose MS, Wright AF;
 DR WPI: 95-215262/28.
 DR N-PDSB: 094036.
 PT Antigen binding structures containing CDRs recognising the CA55.1
 PT antigen - produced by hybridomas and host cells, for use in the
 PT diagnosis and therapy of cancer
 PS Disclosure; Fig.16; 121pp; English.
 CC Mab 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
 CC antigen CA55.1. cDNAs for the heavy (094037) and light (094036)
 CC chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or
 CC v-mu1n humanized 55.1 constructs have been expressed in myeloma
 CC cells and E. coli.
 CC Sequence 239 AA;
 SQ

Query Match 86.7%; Score 818; DB 1; Length 239;
 Best Local Similarity 84.8%; Pred. No. 1,52e-51;

Matches 112; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

DB 1 MDSQAOVLILLILMWSGTCDIYMSQSPSSLAWSAGEKVTMSCKSSQSILNSTRKNYLA 60
 |||||
 QY 1 MDSQAOVLILLILMWSGTCDIYLTQSPDLAVSLGERATISCKSSQSILNSTRKNYLA 60
 |||||
 DB 61 WYQKRGQSPKLLIYASRTSGVDPDRFGSGSGGTDTLTISLSLAEDVAVYCTQSYNL 120
 |||||
 QY 61 WYQKRGQSPKLLIYASRTSGVDPDRFGSGSGGTDTLTISLSLAEDVAVYCTQSYNL 120
 |||||
 DB 121 RTFGGCTKLEIK 132
 |||||
 QY 121 RTFGGCTKVEIK 132

RESULT 3
 ID W10545 standard; Protein; 137 AA.
 AC W10545;

DT 25-SEP-1997 (first entry)
 DE Humanised murine anti-E-selectin antibody CY1788V(LA).
 KW Humanised; murine; mouse; E-selectin; antibody; light chain;
 KW variable region; detection; inhibition; mediation; cell adhesion;
 KW diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
 KW acute respiratory distress syndrome; gross cystic breast disease;
 KW cancer; treatment; splanchic occlusion shock; psoriasis;
 KW complement; chimeric.
 OS Chimeric - Mus spp.
 OS Chimeric - Homo sapiens.
 OS Synthetic.
 PN W09640942-A1.
 PD 19-DEC-1996.
 PF 06-JUN-1996; U09204.
 PR 07-JUN-1995; US-482112.
 PA (CYTE-) CYTEL CORP.
 PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;
 PI Jones S;
 PI WPI: 97-077272/07.
 DR WPI: 97-077272/07.
 DR N-PDSB: T60730.
 PT Humanised anti-E-selectin antibody - useful for diagnosis and
 PT treatment of, e.g. inflammatory responses, septic shock, acute

PT respiratory distress syndrome or cancer
 PS Claim 18; Page 71; 89pp; English.
 CC The present sequence is the humanised murine anti-E-selectin
 CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can
 CC be used to detect E-selectin, or inhibit E-selectin mediated cell
 CC adhesion. It can also be used to diagnose, reduce or inhibit an
 CC inflammatory response, or the severity of pathologies, e.g. septic
 CC shock, acute respiratory distress syndrome, wound associated
 CC sepsis, gross cystic breast disease or cancer, or treat, e.g.
 CC splanchic occlusion shock, or psoriasis. It can be administered to
 CC a human without inducing an immune response. In addition, the
 CC effector portion of the Ab can interact with various components of
 CC the human immune system, including complement.
 CC Sequence 137 AA;
 SQ

Query Match 85.2%; Score 803; DB 1; Length 137;
 Best Local Similarity 85.0%; Pred. No. 2.11e-50;

Matches 113; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

DB 5 MESQPOVLKSLFWVSGTCDIYMTQSPDLAVSLGERATISCKSSQSILNSTRKNYLT 64
 |||||
 QY 1 MDSQAOVLILLILMWSGTCDIYLTQSPDLAVSLGERATISCKSSQSILNSTRKNYLA 60
 |||||
 DB 65 WYQKRGQSPKLLIYASRTSGVDPDRFGSGSGGTDTLTISLSLAEDVAVYCTQSYNL 124
 |||||
 QY 61 WYQKRGQSPKLLIYASRTSGVDPDRFGSGSGGTDTLTISLSLAEDVAVYCTQSYNL 120
 |||||
 DB 125 RTFGGCTKVEIK 137
 |||||
 QY 121 -RTFGGCTKVEIK 132

RESULT 4
 ID W10544 standard; Protein; 137 AA.
 AC W10544;

DT 25-SEP-1997 (first entry)
 DE Humanised murine anti-E-selectin antibody CY1788V(LA).
 KW Humanised; murine; mouse; E-selectin; antibody; light chain;
 KW variable region; detection; inhibition; mediation; cell adhesion;
 KW diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
 KW acute respiratory distress syndrome; gross cystic breast disease;
 KW cancer; treatment; splanchic occlusion shock; psoriasis;
 KW complement; chimeric.
 OS Chimeric - Mus spp.
 OS Chimeric - Homo sapiens.
 OS Synthetic.
 PN W09640942-A1.
 PD 19-DEC-1996.
 PF 06-JUN-1996; U09204.
 PR 07-JUN-1995; US-482112.
 PA (CYTE-) CYTEL CORP.
 PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;
 PI Jones S;
 PI WPI: 97-077272/07.
 DR N-PDSB: T60729.
 PT Humanised anti-E-selectin antibody - useful for diagnosis and
 PT treatment of, e.g. inflammatory responses, septic shock, acute
 PT respiratory distress syndrome or cancer
 PS Claim 17; Page 69; 89pp; English.
 CC The present sequence is the humanised murine anti-E-selectin
 CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can
 CC be used to detect E-selectin, or inhibit E-selectin mediated cell
 CC adhesion. It can also be used to diagnose, reduce or inhibit an
 CC inflammatory response, or the severity of pathologies, e.g. septic
 CC shock, acute respiratory distress syndrome, wound associated
 CC sepsis, gross cystic breast disease or cancer, or treat, e.g.
 CC splanchic occlusion shock, or psoriasis. It can be administered to
 CC a human without inducing an immune response. In addition, the
 CC effector portion of the Ab can interact with various components of
 CC the human immune system, including complement.
 CC Sequence 137 AA;
 SQ

Query Match 84.5%; Score 797; DB 1; Length 137;

PE 14-MAY-1996; U06804.
 PR 15-MAY-1995; US-440621.
 PA (CEDA-) CEDARS SINAI MEDICAL CENT.
 PI Cramer DY, Makowka L, Wu G;
 DR WPI: 97-011852/01.
 DR N-PSDB: T43415.
 PT Inhibiting xenograft rejection by modifying antigen expression of
 the graft - prevents binding of anti-donor antibody and prolongs
 graft survival
 PS Claim 11: Page 99: 135pp: English.
 CC A polypeptide (W06206) comprises the kappa light chain variable
 region of the LEM rat anti-hamster xenograft monoclonal antibody
 HAK-1. It is encoded by a cDNA clone (T43415) obtd. from a HAK-1
 hybridoma light chain cDNA library; the hybridoma was produced by
 CC fusing spleen cells of a LEM rat that had received a hamster heart
 CC transplant, with rat myeloma cells. Recombinant fragments, e.g.
 CC Fab/2 and Fab', of the antibody block binding of preformed
 CC anti-donor xenograft antibodies in a recipient animal serum to
 CC antigen expressed by endothelial cells of the xenograft, i.e. they
 CC inhibit antibody-mediated rejection, thereby prolonging the
 CC survival of the hamster xenograft in the recipient.
 SQ Sequence 134 AA;

Query Match 81.4%; Score 768; DB 1; Length 134;
 Best Local Similarity 78.8%; Pred. No. 9,72e-48;
 Matches 104; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

DB 1 MESQTOYLMILLVNVCSDIYMTOPSSQAVSAGEKVTMSCKSSOSLLYNNKKNYLA 60
 QY 1 MDSQAOYLILLLVNSGCGDIYLTQSPDSLAVSLGERATISCKSSOSLLNSTRRENYLA 60
 DB 61 WYQKPGQSPKLLIYMASTRSGVPPDRFSGSGGTDEFTLTISVQAEDLAVYYCCQYYNL 120
 QY 61 WYQKPGQSPKLLIYMASTRSGVPPDRFSGSGGTDEFTLTISVQAEDVAVYYCTQSYNL 120
 DB 121 YTFGAGTKLEIK 132
 QY 121 YTFGQGTKEIK 132

RESULT 8
 ID R85909 standard; Protein: 133 AA.
 AC R85909;
 DT 02-JUL-1996 (first entry)
 DE Monoclonal antibody, CB-Hep.1, light chain variable domain.
 KM HBV; hepatitis B virus surface antigen; monoclonal; antibody;
 KM CB-Hep.1; immunopurification; detection; hybridoma; recombinant;
 KW Fv; variable; VH; HBSAg.
 OS Mus sp.
 FH Key
 FT peptide 1. .20 Location/Qualifiers
 FT /label= sig_peptide
 FT protein 21..133
 FT /label= mat_protein
 FT domain 21..43
 FT /label= FR1
 FT domain 44..60
 FT /label= CDR1
 FT domain 61..75
 FT /label= FR2
 FT domain 76..82
 FT /label= CDR2
 FT domain 83..114
 FT /label= FR3
 FT domain 115..123
 FT /label= CDR3
 FT domain 124..133
 FT /label= FR4
 FT domain
 PE 686696-A1.
 PD 13-DEC-1995.
 PR 08-JUN-1995; 201535
 PR 09-JUN-1994; CU-000073.
 PA (INGG-) CENT ING GENETICA e BIOTECNOLOGIA.

PA (KAMB/) KAMBEEL R W.
 PI Ayala Avila MA, Cansan-Haden Frias LM, del Carmen Dominguez Horta MC;
 PI Fernandez de Cossio Dorta-Duque ME, Gavilondo Cowley JVG;
 DR WPI: 96-021914/03.
 DR N-PSDB: 074067.
 PT New recombinant single chain Fv antibody fragment - useful for
 PT immuno-purificn. and detection of HBSAg
 PS Claim 1; Page 19: 23pp: English.
 CC R85908 and R85909 are the heavy and light chain variable domains of
 CC the murine hybridoma-derived monoclonal antibody CB-Hep.1 Fv region.
 CC The heavy and light chain regions are used to produce a recombinant
 CC antibody fragment having specificity for the hepatitis B virus
 CC surface antigen (HBSAg). The recombinant antibody may be used for
 CC immunopurification of HBSAg, in immunoassays for the detection of
 CC HBSAg and for insolubilisation of heterologous fusion proteins
 CC expressed in E. coli aiding their purification.
 SQ Sequence 133 AA;

Query Match 80.8%; Score 762; DB 1; Length 133;
 Best Local Similarity 78.2%; Pred. No. 2,78e-47;
 Matches 104; Conservative 15; Mismatches 13; Indels 1; Gaps 1;

DB 1 MDSQAOYLILLLVNSGCGDIYMSQSPSSLAVSVEKVALSCKSSOSLLYNNKKNYLA 60
 QY 1 MDSQAOYLILLLVNSGCGDIYLTQSPDSLAVSLGERATISCKSSOSLLNSTRRENYLA 60
 DB 61 WFOOKPGQSPKLLIYMASTRDSGVPPDRFSGSGGTDEFTLTISVKAEDLAVYYCCQYYNL 120
 QY 61 WYQKPGQSPKLLIYMASTRSGVPPDRFSGSGGTDEFTLTISVQAEDVAVYYCTQSYNL 120
 DB 121 PYTFGGGKLEIK 133
 QY 121 -YTFGQGTKEIK 132

RESULT 9
 ID R28809 standard; Protein: 241 AA.
 AC R28809;
 DT 02-APR-1993 (first entry)
 DE Vector pMDR1007.
 KM Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;
 KM pMDR986; BglII; pMDR1003; J4221(Iq); E. coli; ampicillin resistance;
 KM NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;
 KM melting agarose; immunoglobulin; kappa chain; signal peptide; LC;
 KM humanised; 5A8; light chain; variable region; LV; genomic; constant
 KM antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+;
 KM lymphocyte; helper; inducer; HIV; syncytia; formation.
 KW Synthetic.
 OS Synthetic.
 FH Key
 FT peptide 1. .22 Location/Qualifiers
 FT /note= "Immunoglobulin kappa chain signal peptide"
 FT region 23..134
 FT /note= "Humanised 5A8 LV"
 FT region 135..241
 FT /note= "Human kappa chain LC"
 WT0920305-A.
 PN 11-JUN-1992.
 PD 27-NOV-1991; U08843.
 PR 27-NOV-1990; US-618542.
 PA (BIOU) BIOGEN INC.
 PI Burkly LC, Chisholm PL, Rosa JT, Rosa MD, Thomas DW;
 DR WPI: 92-398399/48.
 DR N-PSDB: 030920.
 PT New anti-CD4 antibody homologues - which bind CD4, do not block
 PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
 PT formation between CD4+ cells
 PS Disclosure: Page 166-7; 205pp: English.
 CC The sequence given is encoded by the insert of the vector pMDR1007.
 CC pMDR1006 (see Q30919) and pSAB132 (see Q30906) were used in the
 CC construction of this vector. Three fragments were ligated together
 CC to generate pMDR1006; a 572 bp fragment of pMDR985 (see Q30913), a
 CC 3442bp AatII/EcoRV fragment of pMDR986 (see Q30918) and a 326 bp
 CC EcoRV/BglII fragment of pMDR1003 (see Q30900). The ligation mixture

DR WPI: 97-334904/31.
DR N-PSDB: T72238.
PT Humanised form of murine monoclonal antibody Mab 15 - useful for
PT treating lung cancer
PS Claim 14; Fig 1; 71pp; English.
CC This polypeptide comprises the light chain variable region VL
CC of murine monoclonal antibody (Mab) 15 (DSM ACC2117), a Mab that
CC shows a therapeutic effect on human tumour cells, especially human
CC lung cancer. Its sequence was deduced from an isolated cDNA
CC clone (see T7238). The Mab 15 VH region sequence (W21654)
CC has also been determined. Amplified VL and VH cDNA sequences were
CC used in a claimed process for the production of novel humanised,
CC reshaped Mab 15 having humanised, reshaped VL and VH regions (see
CC W21651 and W21652), which can be used for treating tumours,
CC especially lung cancer, and for the manufacture of a drug related
CC to tumours, especially lung cancer.
S0 Sequence 137 AA;

5 MESHVLIMLLILMWSTCGDIVMSQSPSSSLVSVGEKTKMCKSSQSLIVSSNKNYLA 64
 Query Match 78.6% Score 741; DB 1; Length 137;
 Best Local Similarity 77.6% Pred. No.1.09e-45;
 Matches 104; Conservative 15; Mismatches 12; Indels 3; Gaps 2

[illegible]

Db 65 WQOQKPGSGPELLLYVMSTRESSGVPDPSGSGSTDDTLTTSYKADDPANVYQQQ YSN 123
 ||||| :
 Oy 61 WYQKPGGPELLLYVMSTRESSGVPDRPSGSGSTDTLTTSIQADDAVAVYCTQSYNL 120
 ||||| :
 Db 124 YPPTGGGCTKLEIK 137

```

Db      124 YPPTFGGGTKEIK 137
      |  |||  |||: |||
Qy      121 Y--TFGGTKEIK 132

```

Search completed: Mon Aug 7 19:03:56 2000
Job time : 14 secs.

(TM)

Distribution rights by Oxford Molecular Ltd

msprch_pp protein - protein database search, using Smith-Waterman algorithm

```
Run on:      Mon Aug 7 19:05:17 2000;  MasPar time 6.96 Seconds
            373 650 M411400 2001 updated/secs
```

tabular output not generated.

```

Title:
>US-09-249-011-8
Description:
(1-132) from PS09249011 non

```

Sequence: 1 MDSQAOVLILLWVGTCG... YCTOSYNTYTEGOGTKVEIK 132

Scoring table: PAM 150

Searched: 145341 seqs, 14437480 residues

Listing first 45 summaries

1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 28.955; Variance 168.930; scale 0.171

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	818	86.7	239	1	US-08-353-	Sequence 37, Applicant 1	2.7ie-49
2	756	80.2	241	2	US-07-916-	Sequence 56, Applicant 1	8.2ie-45
3	739	78.4	133	2	US-08-822-	Sequence 12, Applicant 1	1.38e-43
4	733	77.7	133	4	PCr-US93-1	Sequence 2, Applicant 1	3.75e-43
5	711	75.4	133	4	PCr-US93-1	Sequence 9, Applicant 1	1.44e-41
6	698	74.0	133	4	PCr-US93-1	Sequence 2, Applicant 1	1.25e-40
7	697	72.9	495	3	US-08-828-	Sequence 4, Applicant 1	1.47e-40
8	686	72.7	155	3	US-08-828-	Sequence 11, Applicant 1	9.10e-40
9	686	72.7	342	3	US-08-828-	Sequence 6, Applicant 1	9.10e-40
10	676	71.7	114	1	US-08-360-	Sequence 6, Applicant 1	4.77e-39
11	676	71.7	114	2	US-09-017-	Sequence 6, Applicant 1	4.77e-39
12	676	71.7	114	2	US-08-450-	Sequence 6, Applicant 1	4.77e-39
13	676	71.7	114	2	US-09-014-	Sequence 6, Applicant 1	4.77e-39
14	675	71.6	113	4	PCr-US93-0	Sequence 8, Applicant 1	5.63e-39
15	668	70.8	113	4	PCr-US93-0	Sequence 6, Applicant 1	1.79e-38
16	665	70.5	112	1	US-07-942-	Sequence 30, Applicant 1	2.95e-38
17	664	70.4	219	1	US-08-353-	Sequence 34, Applicant 1	3.44e-38
18	660	70.0	133	4	PCr-US93-1	Sequence 10, Applicant 1	6.74e-38
19	651	69.0	120	1	US-08-026-	Sequence 4, Applicant 1	2.99e-37
20	646	68.5	265	2	US-08-403-	Sequence 16, Applicant 1	6.83e-37
21	645	68.4	113	4	PCr-US95-1	Sequence 21, Applicant 1	8.05e-37
22	645	68.4	113	1	US-08-670-	Sequence 21, Applicant 1	8.05e-37
23	645	68.4	113	1	US-08-667-	Sequence 21, Applicant 1	8.05e-37

24	645	68.4	113	2	US-08-940-	Sequence 21, Applicant	8.05e-37
25	645	68.4	113	1	US-08-940-	Sequence 21, Applicant	8.05e-37
26	635	67.3	109	2	US-08-308-	Sequence 23, Applicant	4.20e-36
27	621	65.9	147	2	US-08-860-	Sequence 8, Applicant	4.24e-35
28	620	65.7	113	4	PT-US93-1	Sequence 5, Applicant	5.01e-35
29	619	65.6	112	2	US-07-916-	Sequence 15, Applicant	5.90e-35
30	608	64.5	182	2	US-08-860-	Sequence 10, Applicant	3.63e-34
31	608	64.5	301	2	US-08-661-	Sequence 14, Applicant	3.63e-34
32	608	64.5	553	2	US-08-661-	Sequence 16, Applicant	5.04e-34
33	606	64.3	129	2	US-08-480-	Sequence 4, Applicant	5.04e-34
34	606	64.3	258	2	US-08-860-	Sequence 13, Applicant	5.04e-34
35	605	64.2	113	1	US-08-470-	Sequence 46, Applicant	5.95e-34
36	605	64.2	113	4	PT-US95-1	Sequence 46, Applicant	5.95e-34
37	605	64.2	113	4	PT-US95-1	Sequence 46, Applicant	5.95e-34
38	605	64.2	113	2	US-08-940-	Sequence 46, Applicant	5.95e-34
39	605	64.2	113	1	US-08-461-	Sequence 46, Applicant	5.95e-34
40	605	64.2	553	2	US-08-265-	Sequence 9, Applicant	5.95e-34
41	605	64.2	553	2	US-08-263-	Sequence 7, Applicant	5.95e-34
42	604	64.1	113	4	PT-US93-1	Sequence 4, Applicant	7.01e-34
43	603	63.9	132	1	US-08-477-	Sequence 91, Applicant	8.27e-34
44	603	63.9	132	1	US-08-477-	Sequence 91, Applicant	8.27e-34
45	603	63.9	132	2	US-08-472-	Sequence 91, Applicant	8.27e-34

ALIGNMENTS

[illegible]


```

Db      61 WYQOKPQSPKLLIYMASTRESGVDPDRFTGSGSDTFTLTISVKAEDLAVYVCOQYYS 120
QY      61 WYQOKPQSPKLLIYMASTRESGVDPDRFTGSGSDTFTLTISLQADVAVYVCTGOSTNL 120
Db      121 PLTFGAGTKVLWK 133
QY      121 -YTFGGGTKEVEIK 132

RESULT      4      STANDARD;      PRT;      133 AA.
ID      PCT-US93-11611-2
XX      AC      xxxxxx
XX      DT
XX      DE      Sequence 2, Application PC/TUS9311611
CC      CC      Sequence 2, Application PC/TUS9311611
CC      CC      GENERAL INFORMATION:
CC      CC      APPLICANT: Co. Man Sung
CC      CC      APPLICANT: Landolfi, Nicholas F.
CC      CC      TITLE OF INVENTION: Humanized Antibodies Reactive with CD18
CC      CC      NUMBER OF SEQUENCES: 11
CC      CC      CORRESPONDENCE ADDRESS:
CC      CC      ADDRESSEE: Townsend and Townsend Kourie and Crew
CC      CC      STREET: One Market Plaza, Steuart Tower, Suite 2000
CC      CC      CITY: San Francisco
CC      CC      STATE: California
CC      CC      COUNTRY: USA
CC      CC      ZIP: 94105
CC      CC      COMPUTER READABLE FORM:
CC      CC      MEDIUM TYPE: Floppy disk
CC      CC      COMPUTER: IBM PC compatible
CC      CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      CC      SOFTWARE: Patent In Release #1.0, Version #1.25
CC      CC      CURRENT APPLICATION DATA:
CC      CC      APPLICATION NUMBER: PCT/US93/11611
CC      CC      FILING DATE: 30-NOV-1993
CC      CC      CLASSIFICATION:
CC      CC      PRIOR APPLICATION DATA:
CC      CC      APPLICATION NUMBER: US 07/983,949
CC      CC      FILING DATE: 01-DEC-1992
CC      CC      ATTORNEY/AGENT INFORMATION:
CC      CC      NAME: Smith, William M.
CC      CC      REGISTRATION NUMBER: 30,223
CC      CC      REFERENCE/DOCKET NUMBER: 11823-45
CC      CC      TELECOMMUNICATION INFORMATION:
CC      CC      TELEPHONE: 415-326-2400
CC      CC      TELEFAX: 415-326-2422
CC      CC      INFORMATION FOR SEQ. ID NO: 2:
CC      CC      SEQUENCE CHARACTERISTICS:
CC      CC      LENGTH: 133 amino acids
CC      CC      TYPE: amino acid
CC      CC      TOPOLOGY: linear
CC      CC      MOLECULE TYPE: protein
CC      CC      SEQUENCE 133 AA; 14459 MW; 109715 CN;

Query Match      77.7%;      Score 733;      DB 4;      Length 133;
Best Local Similarity 76.7%;      Pred. No. 3.75e-43;
Matches 102;      Conservative 18;      Mismatches 12;      Indels 1;      Gaps 1;

Db      1 MDSOAQVILMLLLWVSGCDIVMSGSSPLSLAVSGEKVPMSCSSOSLLAVSGEKV 60
QY      1 MDSOAQVILMLLLWVSGCDIVLQSPDSLAVSGERATSSOSLSRFRRENYLA 60
Db      61 WYQOKPQSPKLLIYMASTRESGVDPDRFTGSGSDTFTLTISVKAEDLAVYVCOQYYS 120
QY      61 WYQOKPQSPKLLIYMASTRESGVDPDRFTGSGSDTFTLTISLQADVAVYVCTGOSTNL 120
Db      121 PLTFGSGTKLEIK 133
QY      121 -YTFGGGTKEVEIK 132

```

OY		121	-YTFGGGKVEIK	132	
RESULT	5		STANDARD;	PRT;	133 AA.
ID	PCT-US93-11612-2				
XX	xxxxxx				
XX					
DT					
DE					
XX					
CC	Sequence 2, Application PC/TUS9311612				
CC	Sequence 2, Application PC/TUS9311612				
CC	GENERAL INFORMATION:				
CC	APPLICANT: Co, Man Sung				
CC	TITLE OF INVENTION: Humanised Antibodies Reactive with				
CC	TITLE OF INVENTION: L>Selectin				
CC	NUMBER OF SEQUENCES: 12				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: Townsend and Townsend Kourie and Crew				
CC	STREET: One Market Plaza, Stewart Tower, Suite 2000				
CC	CITY: San Francisco				
CC	STATE: California				
CC	COUNTRY: USA				
CC	ZIP: 94105				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	COMPUTER: IBM PC compatible				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: PCT/US93/11612				
CC	FILING DATE:				
CC	CLASSIFICATION:				
CC	Prior APPLICATION DATA:				
CC	APPLICATION NUMBER: US 07/983,946				
CC	FILING DATE: 01-DEC-1992				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: Smith, William M.				
CC	REGISTRATION NUMBER: 30,223				
CC	REFERENCE/DOCKET NUMBER: 11823-22				
CC	TELECOMMUNICATION INFORMATION:				
CC	TELEPHONE: 415-326-2400				
CC	TELEFAX: 415-326-2422				
CC	INFORMATION FOR SEQ ID NO: 2:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 133 amino acids				
CC	TYPE: amino acid				
CC	TOPOLOGY: linear				
CC	MOLECULE TYPE: protein				
SQ	SEQUENCE 133 AA; 14546 MW; 100454 CN;				
Query Match	75.4%;	Score 711;	DB 4;	Length 133;	
Best Local Similarity	72.9%;	Pred. No. 1,44e-41;			
Matches 97;	Conservative 22;	Mismatches 13;	Indels 1;	Gaps 1,	
Db	1 MESQTQVLMFFLLWVSACADIVWTQSPSSFLAMSVGVKVTYTKCSSQSLSLNOKNYIA 60				
OY	1 MDSQAQYVILLILLYMWSGCGSDIVLTQSPDSLAVSLGERATISCSNSSLNRRENTYA 60				
Db	61 WYQQKPGQSPRLYLVAFTSRSGVPDRFETGSGLTDETLTISSVQADLADYPFCQHYST 120				
OY	61 WYQQKPGQSPRLILYMASTRSGVPPDRSRGSGSCTDFTLTISLQADVAVNYCTQSYNL 120				
Db	121 PLITGAGTKLEK 133				
OY	121 -YTFGGGKVEIK 132				
RESULT	6		STANDARD;	PRT;	133 AA.
ID	PCT-US93-11611-9				
XX	xxxxxx				
CC					

[illegible]

```
CC CC GENERAL INFORMATION:
CC CC APPLICANT: Koentgen, Frank
CC CC APPLICANT: Suess, Gabriele M.
CC CC APPLICANT: Tarlinton, David M.
CC CC APPLICANT: Treutlein, Herbert R.
CC CC TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
CC CC TYPE OF INVENTION: PRODUCING SAME
CC CC NUMBER OF SEQUENCES: 14
CC CC CORRESPONDENCE ADDRESS:
CC CC ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
CC CC STREET: 400 Garden City Plaza
CC CC CITY: Garden City
CC CC STATE: New York
CC CC COUNTRY: United States of America
CC CC ZIP: 11530
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: Floppy disk
CC CC COMPUTER: IBM PC compatible
CC CC OPERATING SYSTEM: PC-DOS/MS-DO5
CC CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: US/08/828,741B
CC CC FILING DATE: 26-MAR-1997
CC CC CLASSIFICATION: 435
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: Digiglo, Frank S.
CC CC REGISTRATION NUMBER: 31,346
CC CC REFERENCE/DOCKET NUMBER: 10591
CC CC TELECOMMUNICATION INFORMATION:
CC CC TELEPHONE: (516) 742-4343
CC CC TELEFAX: (516) 742-4366
CC CC TELEX: 230 901 SANS UR
CC CC INFORMATION FOR SEQ ID NO: 4:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 495 amino acids
CC CC TYPE: amino acid
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
CC CC SEQUENCE 495 AA; 51894 MW; 1309376 CN;
SQ
Query Match 73.9%; Score 697; DB 3; Length 495;
Best Local Similarity 85.6%; Pred. No. 1,47e-40;
Matches 101; Conservative 6; Mismatches 10; Indels 1; Gaps 1.
Db 365 SGGGGDIYMTOSPDSLAVSLGERATINCKSSQSVLYSNSKNYLAWYOQRPGOPPKLLIY 424
Oy 16 SGTGCDIYLTQSPDLSLWGLGERATISCKSSQSLSLNRTRENTLAWYQKRGOPPKLLIY 75
Db 425 WASTRESSVPRPFGSGSGSDTFITITSSLAEDVAIVYYCOQYSTPSFGCGTKLEIK 482
Oy 76 WASTRESSVPFRFGSGSGSDTFITITSSLAEDVAIVYYCTQSYNL-YTFGCGTRVEIK 132
RESULT 8
ID US-08-828-741B-11 STANDARD; PRT: 155 AA.
XX AC xxxxxx
XX DT |
XX XX |
DE Sequence 11, Application US/08828741B
CC XX |
CC Sequence 11, Application US/08828741B
CC Patent No. 6043069
CC GENERAL INFORMATION:
CC APPLICANT: Koentgen, Frank
CC APPLICANT: Suess, Gabriele M.
CC APPLICANT: Tarlinton, David M.
CC APPLICANT: Treutlein, Herbert R.
CC TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
CC TYPE OF INVENTION: PRODUCING SAME
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
```

CC	ADDRESS: SCULLY, SCOTT MURPHY & PRESSER	DB 3;	Length 155;
CC	STREET: 400 Garden City Plaza		
CC	CITY: Garden City		
CC	STATE: New York		
CC	COUNTRY: United States of America		
CC	ZIP: 11530		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/828,741B		
CC	FILING DATE: 26-MAR-1997		
CC	CLASSIFICATION: 435		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Digiglio, Frank S.		
CC	REGISTRATION NUMBER: 31,346		
CC	REFERENCE/DOCKET NUMBER: 10591		
CC	TELEPHONE: (516) 742-4343		
CC	TELEFAX: (516) 742-4366		
CC	INFORMATION FOR SEQ ID NO: 11:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 155 amino acids		
CC	TYPE: amino acid		
CC	TOPOLOGY: linear		
CC	MOLECULE TYPE: protein		
CC	SEQUENCE 155 AA; 16932 MW; 135999 CN;		
CC	Query Match 72.7%; Score 686; DB 3; Length 155;		
CC	Best Local Similarity 86.7%; Pred. No. 9.10e-40;		
CC	Matches 98; Conservative 6; Mismatches 8; Indels 1; Gaps 1;		
DB	30 DIVATQSPDLSAVSIGEATINCKSSQSVLSSSKNYLWYQKPGQPKLLIYMASTR 89		
QY	21 DIVLTQSDSLAVSIGEATISCKSSQSVLSSSKNYLWYQKPGQPKLLIYMASTR 80		
DB	90 ESGVPDFRSGSGSGTDFLTLLTSSLAQAEADVAVYYCQYYSPFYSFGQGTLEIK 142		
QY	81 ESGVPDFRSGSGSGTDFLTLLTSSLAQAEADVAVYYCTQSYNL-YTGGQGTKEIK 132		
RESULT	9 STANDARD; PRT; 342 AA.		
ID	US-08-828-741B-6		
XX	AC	xxxxxx	
DT	Sequence 6, Application US/08828741B		
DE	Sequence 6, Application US/08828741B		
XX	Patent No. 6043069		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Koentgen, Frank		
CC	APPLICANT: Suess, Gabriele M.		
CC	APPLICANT: Tarlington, David M.		
CC	APPLICANT: Trentlein, Herbert R.		
CC	TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF		
CC	NUMBER OF SEQUENCES: 14		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER		
CC	STREET: 400 Garden City Plaza		
CC	CITY: Garden City		
CC	STATE: New York		
CC	COUNTRY: United States of America		
CC	ZIP: 11530		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		

```

CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.30
CC
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/828,741B
CC      FILING DATE: 26-MAR-1997
CC      CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Digiglio, Frank S.
CC      REGISTRATION NUMBER: 31,346
CC      REFERENCE/DOCKET NUMBER: 10591
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (516) 742-4343
CC      TELEFAX: (516) 742-4366
CC      TELEX: 230 901 SANS UR
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 342 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 342 AA; 36371 MW; 598487 CN;
SQ
Query Match          72.7%; Score 686; DB 3; Length 342;
Best Local Similarity 86.7%; Pred. No. 9, 10e-40;
Matches 98; Conservative 6; Mismatches 8; Indels 4; Gaps 1;
Db      30 DIVMTQSPDSLAVSGERATINCKSSQSVLYSSNKNTLAWYQKRPQPKLLTQVASTR 89
Qy      21 DIVLQSPDSLAVSGERATISCKSSQSLSRTRNTRENTLAWYQKRPQPKLLITVASTR 80
Db      90 ESGVDRSGSGSGTFTLTISSLQAEDEVAVYYCCQYVSTPYSFQSGKRLK 124
Qy      81 ESGVDRSGSGSGTFTLTISSLQAEDEVAVYYCYQSYNL-YTFGQGTQVKEIK 122
RESULT 10
ID      US-08-360-125-6          STANDARD;          PRT;          114 AA.
XX      xxxxxx
XX
XX      Sequence 6, Application US/08360125
XX
CC      Sequence 6, Application US/08360125
CC      Patent No. 5767246
CC      GENERAL INFORMATION:
CC      APPLICANT: Saijo HOSOKAWA
CC      APPLICANT: Toshiaki TAGAWA
CC      APPLICANT: Yoko HIRAKAWA
CC      APPLICANT: No. 5767246Ihiko ITO
CC      APPLICANT: Kazuhiro NAGAIKE
CC      TITLE OF INVENTION: Human Monoclonal Antibody
CC      TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
CC      TITLE OF INVENTION: Cell Membrane
CC      NUMBER OF SEQUENCES: 42
CC      CORRESPONDENCE ADDRESSES:
CC      ADDRESSEE: Wenderoth, Lind & Ponack
CC      STREET: 805 Fifteenth Street, N.W., #700
CC      CITY: Washington
CC      STATE: D.C.
CC      COUNTRY: U.S.A.
CC      ZIP: 20005
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
CC      COMPUTER: IBM Compatible
CC      OPERATING SYSTEM: MS-DOS
CC      SOFTWARE: WordPerfect 5.1
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/360,125
CC      FILING DATE:
CC      CLASSIFICATION: 424
CC      PRIOR APPLICATION DATA:
CC

```

```

CC APPLICATION NUMBER: 07/905,554
CC FILING DATE: June 29, 1992
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Warren M. Cheek, Jr.
CC REGISTRATION NUMBER: 33,367
CC REFERENCE/DOCKET NUMBER:
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-371-8830
CC TELEFAX:
CC
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 114 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC HYPOTHEetical:
CC ANTI-SENSE:
CC FRAGMENT TYPE:
CC ORIGINAL SOURCE:
CC ORGANISM:
CC STRAIN:
CC INDIVIDUAL ISOLATE:
CC DEVELOPMENTAL STAGE:
CC HAPLOTYPE:
CC TISSUE TYPE:
CC CELL TYPE: Hybridoma producing human
CC CELL LINE: antibody GAH
CC ORGANELLE:
CC IMMEDIATE SOURCE:
CC LIBRARY:
CC CLONE:
CC POSITION IN GENOME:
CC CHROMOSOME/SEGMENT:
CC MAP POSITION:
CC UNITS:
CC FEATURE:
CC NAME/KEY:
CC LOCATION:
CC IDENTIFICATION METHOD:
CC OTHER INFORMATION:
CC PUBLICATION INFORMATION:
CC AUTHORS:
CC TITLE:
CC JOURNAL:
CC VOLUME:
CC ISSUE:
CC PAGES:
CC DATE:
CC DOCUMENT NUMBER:
CC FILING DATE:
CC PUBLICATION DATE:
CC RELEVANT RESIDUES IN SEQ ID NO:
CC SEQUENCE 114 AA; 12731 MW; 76848 CN;
CC
CC Query Match 71.7%; Score 676; DB 1; Length 114;
CC Best Local Similarity 85.8%; Pred.No.4,77e-39;
CC Matches 97; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
CC
Db 1 DIVVMSQPSDLAVSLGERATINCASSQSQSVLYNSNNKITYLAWYQOKPCQPPKLLIYMASTR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 21 DIVVQSSDSLAVSLGERATISCKSSOSLNSRTRENYLAWYQOKPCQPPKLLIYMASTR 80
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 ESGVDFRSGSGSGTDFLTITSSLQAEVAVAYYCOQXYSTPWPTRGGGTKEIK 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
81 ESGVDFRSGSGSGTDFLTITSSLQAEVAVAYYCTQSYNL-YTFGGGTKEIK 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 11

```

ID	US-09-017-628-6	STANDARD:	PRT:	114 AA.
XX	xxxxxx			
XX				
XX				
XX				
DE	Sequence 6, Application US/09017628			
CC				
CC	Sequence 6, Application US/09017628			
CC	Patent No. 5990287			
CC	GENERAL INFORMATION:			
CC	APPLICANT: HOSOKAWA, Saito			
CC	APPLICANT: TAKAWA, Toshiaki			
CC	APPLICANT: HIRAKAWA, Yoko			
CC	APPLICANT: ITO, No. 5990287h1h1ko			
CC	APPLICANT: NAGAIKE, Kazuhiro			
CC	TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO			
CC	TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE			
CC	FILE REFERENCE: 177/527361KH			
CC	CURRENT APPLICATION NUMBER: US/09/017, 628			
CC	CURRENT FILING DATE: 1998-02-02			
CC	EARLIER APPLICATION NUMBER: 08/560,125			
CC	EARLIER FILING DATE: 1994-12-20			
CC	NUMBER OF SEQ ID NOS: 42			
CC	SOFTWARE: PatentIn Ver. 2.0			
CC	SEQ ID NO 6			
CC	LENGTH: 114			
CC	TYPE: PRT			
CC	ORGANISM: Unknown			
CC	FEATURE:			
CC	OTHER INFORMATION: Hybridoma producing human antibody GAH			
SO	SEQUENCE 114 AA: 12731 MW: 76848 CN:			

```

Query Match          71.7%: Score 676; DB 2; Length 114;
Best Local Similarity 85.8%; Pred. No. 4,77e-39;
Matches 97; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Dd      1 DIVATGSPDSLAVLSLEERATINCKSSQSVLYVNSNNKKIYAWOOPGCPKLLYYMSTR 60
        |||:|||||||:|||||:|||||:|:|:|||||||:|||||
Oy      21 DIVLTGSPDSLAVLSGERATISCKSSQSILNRTENTLANTYQAKPGCPPKLLYYMSTR 80
        |||:|||||||:|||||:|||||:|:|:|||||||:|||||

Db      61 EGGVPDRFSGSGSGETFTLTITSLQAEDYAVYYCOQYISTPWFEGGTKEIK 13
        |||:|||||||:|||||:|||||:|:|:|||||||:|||||
Oy      81 EGGVDRFSGSGSGETFTLTITSLQAEDYAVYYCTQSYTNL-YTIGQGKTVEIK 32
        |||:|||||||:|||||:|||||:|:|:|||||||:|||||

RESULT   12
ID       US-08-450-578-6         STANDARD;           PRT;    114 AA.
AC       xxxxxx
XX
XX
XX
XX
XX
DE       Sequence 6, Application US/08450578
XX
CC       Sequence 6, Application US/08450578
CC       Patent No. 5837845
CC       GENERAL INFORMATION:
CC       APPLICANT: Saiko HOSOKAWA
CC       APPLICANT: Toshitaki TAGAMA
CC       APPLICANT: Yoko HIRAKAWA
CC       APPLICANT: No. 5837845 Hiroko ITO
CC       TITLE OF INVENTION: Human Monoclonal Antibody
CC       TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
CC       TITLE OF INVENTION: Cell Membrane
CC       NUMBER OF SEQUENCES: 42
CC       CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Wenderoth, Lind & Ponack
CC       STREET: 805 Fifteenth Street, N.W., #700
CC       CITY: Washington
CC       STATE: D.C.
CC       COUNTRY: U.S.A.

```



```

CC      ZIP: 20005
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
CC      COMPUTER: IBM Compatible
CC      OPERATING SYSTEM: MS-DOS
CC      SOFTWARE: Wordperfect 5.1
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/450,578
CC      FILING DATE: May 25, 1995
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 08/360,125
CC      FILING DATE: December 20, 1994
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/905,534
CC      FILING DATE: June 29, 1992
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Warren M. Cheek, Jr.
CC      REGISTRATION NUMBER: 33,367
CC      REFERENCE/DOCKET NUMBER:
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 202-371-8850
CC      TELEFAX:
CC      TELEX:
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 114 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      HYPOTHETICAL:
CC      ANTI-SENSE:
CC      FRAGMENT TYPE:
CC      ORIGINAL SOURCE:
CC      ORGANISM:
CC      STRAIN:
CC      INDIVIDUAL ISOLATE:
CC      DEVELOPMENTAL STAGE:
CC      HAPLTYPE:
CC      TISSUE TYPE:
CC      CELL TYPE: Hybridoma producing human
CC      CELL LINE: antibody G4H
CC      ORGANELLE:
CC      IMMEDIATE SOURCE:
CC      LIBRARY:
CC      CLONE:
CC      POSITION IN GENOME:
CC      CHROMOSOME/SEGMENT:
CC      MAP POSITION:
CC      UNITS:
CC      FEATURE:
CC      NAME/KEY:
CC      LOCATION:
CC      IDENTIFICATION METHOD:
CC      OTHER INFORMATION:
CC      PUBLICATION INFORMATION:
CC      AUTHORS:
CC      TITLE:
CC      JOURNAL:
CC      VOLUME:
CC      ISSUE:
CC      PAGES:
CC      DATE:
CC      DOCUMENT NUMBER:
CC      FILING DATE:
CC      PUBLICATION DATE:
CC      RELEVANT RESIDUES IN SEQ ID NO:
CC      SEQUENCE 114 AA; 12731 MW; 76848 CN;
Query Match 71.7%; Score 676; DB 2; Length 114;
Best Local Similarity 83.8%; Pred. No. 4,77e-39;

```

```

Matches      97;  Conservative      6;  Mismatches      9;  Indels      1;  Gaps      1;

Db      1  DIVTQSPDLSAVSLGERATINCXSSQSVLYNSNNKYIAMIYQKFGQPKLLIYASTR 60
QY      21  DIVLTQSPDLSAVSLGERATINCXSSQSVLYNSNNKYIAMIYQKFGQPKLLIYASTR 80
Db      61  ESGVPDRSGSGSGTDFLTITSSLAQADVAIVYCCQYYSIPMTFGGTVEIK 113
QY      81  ESGVPDRSGSGSGTDFLTITSSLAQADVAIVYCCQSYNL-YTFGGGTVEIK 132

RESULT      13
ID      US-09-014-880-6      STANDARD;      PRT;      114 AA.
XX      xxxxxx
XX
XX      Sequence 6, Application US/09014880
CC
CC      Sequence 6, Application US/09014880
CC      Patent No. 5990297
CC      GENERAL INFORMATION:
CC      APPLICANT: Saiko HOSOKAWA et al.
CC      TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
CC      TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
CC      NUMBER OF SEQUENCES: 42
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
CC      STREET: 2033 K Street, N.W., #800
CC      CITY: Washington
CC      STATE: D.C.
CC      COUNTRY: U.S.A.
CC      ZIP: 20006
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
CC      COMPUTER: IBM Compatible
CC      OPERATING SYSTEM: MS-DOS
CC      SOFTWARE: Wordperfect 5.1
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/09/014,880
CC      FILING DATE: January 28, 1998
CC      CLASSIFICATION: 536
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 08/450,578
CC      FILING DATE: May 25, 1995
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 08/360,125
CC      FILING DATE: December 20, 1994
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/905,534
CC      FILING DATE: June 29, 1992
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Warren M. Cheek, Jr.
CC      REGISTRATION NUMBER: 33,367
CC      REFERENCE/DOCKET NUMBER:
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 202-721-8200
CC      TELEFAX: 202-721-8250
CC      TELEX:
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 114 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      ORIGINAL SOURCE:
CC      CELL TYPE: Hybridoma producing human
CC      CELL TYPE: antibody GAH
CC      SEQUENCE      114 AA, 12731 MW, 76848 CN;
50

```


Sun Aug 27 09:11:06 2000

US-09-249-011-8.rai
